

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 21:08:15 ; Search time 6122.4 Seconds  
(without alignments)  
10898.153 Million cell updates/sec

Title: US-10-009-852-15  
Perfect score: 1377  
Sequence: 1 atgtcgactactgggacac.....ccctgtctccgggtaaatga 1377

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl.\*  
1: gb\_ba.\*  
2: gb\_htg.\*  
3: gb\_in.\*  
4: gb\_on.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pt.\*  
10: gb\_ro.\*  
11: gb\_scs.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1377	100.0	1377	6	AX056749
2	1328.4	96.5	1453	6	AX056745
3	1049.2	76.2	1444	6	AX056747
4	1039	75.5	1359	6	AX056739
5	1032.4	75.0	1389	6	AX056741
6	987.4	71.7	1674	6	AX056737
7	982.4	71.3	1704	6	AX056743
8	980.8	71.2	1704	6	AX056735
9	687.2	49.9	1383	6	AX138526
10	686	49.8	2043	6	AR112718
11	684	49.7	705	6	AX380678
12	684	49.7	762	6	AX556168
13	684	49.7	1019	6	AR137115
14	684	49.7	1019	6	BD271954
15	684	49.7	1019	6	AR275187
16	684	49.7	1159	9	HSAL7957
17	684	49.7	1182	6	AR173440
18	684	49.7	1182	6	CQ857740
19	684	49.7	1356	6	AX357970

20	684	49.7	1392	6	CQ774324	CQ774324	Sequence
21	684	49.7	1392	6	CQ790351	CQ790351	Sequence
22	684	49.7	1392	6	CQ812157	CQ812157	Sequence
23	684	49.7	1392	6	CQ816433	CQ816433	Sequence
24	684	49.7	1392	6	AX594307	AX594307	Sequence
25	684	49.7	1392	6	AX616608	AX616608	Sequence
26	684	49.7	1392	6	AX616908	AX616908	Sequence
27	684	49.7	1404	6	AX268679	AX268679	Sequence
28	684	49.7	1407	6	AX556959	AX556959	Sequence
29	684	49.7	1407	6	AX709558	AX709558	Sequence
30	684	49.7	1413	6	AX556949	AX556949	Sequence
31	684	49.7	1413	6	AX709548	AX709548	Sequence
32	684	49.7	1422	6	BD013334	BD013334	Novel pep
33	684	49.7	1422	6	BD013336	BD013336	Novel pep
34	684	49.7	1422	6	BD013337	BD013337	Novel pep
35	684	49.7	1422	6	BD013338	BD013338	Novel pep
36	684	49.7	1422	6	BD013340	BD013340	Novel pep
37	684	49.7	1422	9	AB159728	AB159728	Homo sapi
38	684	49.7	1428	6	AR031186	AR031186	Sequence
39	684	49.7	1428	6	AR042591	AR042591	Sequence
40	684	49.7	1428	6	AR059284	AR059284	Sequence
41	684	49.7	1428	6	AR076262	AR076262	Sequence
42	684	49.7	1428	6	AR300619	AR300619	Sequence
43	684	49.7	1431	6	AR108863	AR108863	Sequence
44	684	49.7	1431	6	AR108867	AR108867	Sequence
45	684	49.7	1431	6	E10697	E10697	cdna encodi

ALIGNMENTS

RESULT 1  
AX056749  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS

AX056749  
Sequence 15 from Patent WO0075319.  
AX056749  
AX056749.1 GI:12309728  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Papadopoulos, N.J., Davis, S. and Yancopoulos, G.D.  
Modified chimeric polypeptides with improved pharmacokinetic properties  
Patent: WO 0075319-A 15 14-DEC-2000;  
REGENERON PHARMACEUTICALS, INC. (US)  
Location/Qualifiers  
1. .1377  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
1. .1377  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC22379.1"  
/db\_xref="GI:12309729"  
/translation="MWSYDVTGVLLCALLSCLLTGSSSGSDTGRPFVMSYSEIPEII  
HMTGRELVIPCRVTSPNITVTKKFLDPLTLPDGKRIIWDNRKGIISNATYKEIGL  
LTCEATVNGHLYKTYLTITRQNTIIDVLSPSHGIELSGKDLVNLCTARTLNNGI  
DFNWEYPSKHQKLVNRDLKTOGSEMKKFLSTLTIDGVTRSDQGLYTCASSGLM  
TKNSYFVRVHEKDKTKTCCPAPELGGPSVFLFPKPKDITMI SRTPEVTCVVVD  
VSHDEVKENYVDGVEVHNATKPREEQNYSTRVSVLTVLHQDLNKGKEYCKKV  
SNKALPAPIETKISKAPQPRQVYTLPPSRDELTKNQVSLTCLVKGFTPSDIAVEM  
ESNGQPENNYKTTTPPVLDSGSPFLYSKLTVDKSRWQQGNVFCVSMHEALHNHYTK  
SLSLSPGK"

ORIGIN

Query Match 100.0%; Score 1377; DB 6; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 6.2e-310;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGTGTGGCGCTGCTCAGCTGTCTGCTTCTC 60  
Db |||||  
1 ATGGTCAGCTACTGGGACACCGGGGTCCTGTGTGGCGCTGCTCAGCTGTCTGCTTCTC 60  
QY 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db |||||  
61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
QY 121 CCGAAATTAACAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCA 180  
Db |||||  
121 CCGAAATTAACAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCA 180  
QY 181 CCTAACATCACTGTACTTTTAAAGAGTTTCCACTTGACACTTTTGAATGATGATGGAATA 240  
Db |||||  
181 CCTAACATCACTGTACTTTTAAAGAGTTTCCACTTGACACTTTTGAATGATGATGGAATA 240  
QY 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGCTACAAAGAAATA 300  
Db |||||  
241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGCTACAAAGAAATA 300  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA 360  
Db |||||  
301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAAACTATCTCACA 360  
QY 361 CATCGACAAACCAATACATATGATGTGTTCTGAGTCCGTCTCATGGAATTTGAACATA 420  
Db |||||  
361 CATCGACAAACCAATACATATGATGTGTTCTGAGTCCGTCTCATGGAATTTGAACATA 420  
QY 421 TCTGTGGAGAAAGCTTGTCTTAAATGTACAGCAAGAACTGAACATAAATGTGGGATT 480  
Db |||||  
421 TCTGTGGAGAAAGCTTGTCTTAAATGTACAGCAAGAACTGAACATAAATGTGGGATT 480  
QY 481 GACTTCAACTCGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAACCGAGAC 540  
Db |||||  
481 GACTTCAACTCGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAACCGAGAC 540  
QY 541 CTAAACCCAGTCTGGGAGTGAGATGAGAAATTTTGAACACTTAACTATAGATGGT 600  
Db |||||  
541 CTAAACCCAGTCTGGGAGTGAGATGAGAAATTTTGAACACTTAACTATAGATGGT 600  
QY 601 GTAACCCGAGTGTGACCAAGGATTTGACACCTGTGCGAGCATCCAGTGGGCTGATCACCAG 660  
Db |||||  
601 GTAACCCGAGTGTGACCAAGGATTTGACACCTGTGCGAGCATCCAGTGGGCTGATCACCAG 660  
QY 661 AAGAACAGCATTGTCAGGGTCCATGAAAGGACAAACTCAACATGCCCCACCGTGC 720  
Db |||||  
661 AAGAACAGCATTGTCAGGGTCCATGAAAGGACAAACTCAACATGCCCCACCGTGC 720  
QY 721 CCAGCACTGAACTCTCTGGGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780  
Db |||||  
721 CCAGCACTGAACTCTCTGGGGGACCGTCACTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 780  
QY 781 ACCCTCATGATCTCCCGACCCCTGAGGTCACTGCTGTGGTGGGAGCTGAGCCACGAA 840  
Db |||||  
781 ACCCTCATGATCTCCCGACCCCTGAGGTCACTGCTGTGGTGGGAGCTGAGCCACGAA 840  
QY 841 GACCCTGAGGTCAAGTTCAACTGCTGACGCGGCTGGAGGTCATATGCGCAAGACA 900  
Db |||||  
841 GACCCTGAGGTCAAGTTCAACTGCTGACGCGGCTGGAGGTCATATGCGCAAGACA 900  
QY 901 AAGCCGGGAGGAGCAGTACAAACGACGCTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGT 960  
Db |||||  
901 AAGCCGGGAGGAGCAGTACAAACGACGCTACCGTGTGGTGGTGGTGGTGGTGGTGGTGGT 960  
QY 961 CACCAGGACTGGCTGAATGGCAAGAGTACAAAGTGCAGGTCCTCAACAAAGCCCTCCCA 1020  
Db |||||  
961 CACCAGGACTGGCTGAATGGCAAGAGTACAAAGTGCAGGTCCTCAACAAAGCCCTCCCA 1020  
QY 1021 GCCCCATCGAGAAACCATCTCAAAGCCAAAGGGCAGCCCGAGAACCAACAGGTGTAC 1080  
Db |||||  
1021 GCCCCATCGAGAAACCATCTCAAAGCCAAAGGGCAGCCCGAGAACCAACAGGTGTAC 1080  
QY 1081 ACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACAGGTCAGCTGACCTGCTGGTCTC 1140

Db |||||  
1081 ACCCTGCCCCCATCCCGGGATGAGTGACCAAGAACAGGTCAGCTGACCTGCTGGTCTC 1140  
QY 1141 AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGCGCAGCCGGAAC 1200  
Db |||||  
1141 AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGCGCAGCCGGAAC 1200  
QY 1201 AACTAAGAACACCGCTCCCGTGTGGAATCCGACCGGCTCTTCTTCTTCTTCTTCTTCT 1260  
Db |||||  
1201 AACTAAGAACACCGCTCCCGTGTGGAATCCGACCGGCTCTTCTTCTTCTTCTTCTTCT 1260  
QY 1261 CTACCGTGTGACAGAGCAGTGGCAGCGGGAACGCTCTTCTCATGCTCCGATGCAT 1320  
Db |||||  
1261 CTACCGTGTGACAGAGCAGTGGCAGCGGGAACGCTCTTCTCATGCTCCGATGCAT 1320  
QY 1321 GAGGCTCTGCAACCACTACACGCAAGAGGCTCTCCCTGTCTCCGGGTAATGA 1377  
Db |||||  
1321 GAGGCTCTGCAACCACTACACGCAAGAGGCTCTCCCTGTCTCCGGGTAATGA 1377

RESULT 2  
AX056745  
LOCUS AX056745 1453 bp DNA linear PAT 17-JAN-2001  
DEFINITION Sequence 11 from Patent WO0075319.  
ACCESSION AX056745  
VERSION AX056745.1 GI:12309724  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
REFERENCE  
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.  
TITLE Modified chimeric polypeptides with improved pharmacokinetic  
properties  
JOURNAL Patent: WO 0075319-A 11 14-DEC-2000;  
REGENERON PHARMACEUTICALS, INC. (US)  
FEATURES  
source Location/Qualifiers  
1. .1453  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
69. .1445  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC22377.1"  
/db\_xref="GI:12309725"  
/translation="MYSYMDTGVLLCALLSLILLTGSSSGRPVPMVSEIPIIHT  
EGRELIPKRVTSFNITVILKKPFLDTLIPDKRIIWDNRKFIISNATYKEIGLLTC  
EATVNGHLKYNTYLTHRQNTIIDVLSPHSGIELSVGERKLVNLCRTAEINLVGIDFN  
WEYPSKHQHKLVNRDLKTQSGEMKKFLSTLIDGTVRSDDGLYTCAASSGLMTKK  
NSTFVRVHKPGDKTHTCPPCAPPELLAGPSVFLPPKPKDLMISRTPEVTCVVD  
VSHDEVKFNWTVDGVVHNATKPREOYNSTYRVSVLTVLHODWLNGKVKCV  
SNKALPAPLEKTSKAGQPREQVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEW  
ESNGQENNTKTTTPVLDSDGSFLLSKLITVDSRWQQGNVFCSVWHEALRNHYTK  
SLSLSPGK"

Query Match 96.5%; Score 1328.4; DB 6; Length 1453;  
Best Local Similarity 98.6%; Pred. No. 1.3e-298;  
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;  
QY 1 ATGGTCAGCTACTGGGACACCGGGGTCCTGTGTGGCGCTGCTCAGCTGTCTGCTTCTC 60  
Db 69 ATGGTCAGCTACTGGGACACCGGGGTCCTGTGTGGCGCTGCTCAGCTGTCTGCTTCTC 128  
QY 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db 129 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 179  
QY 121 CCGAAATTAACAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCA 180  
Db 180 CCGAAATTAACAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCAATGATCA 239

```
QY 181 CCTAACATCACTGTTACTTTTAAAGAGTTTCCACTTGCACACTTTGATCCCTGATGAAAA 240
Db 240 CCTAACATCACTGTTACTTTTAAAGAGTTTCCACTTGCACACTTTGATCCCTGATGAAAA 299
QY 241 CGCATATCTGGACAGTAGAAGGGCTTCATCATATCAATATGCAACGTACAAAGAAATA 300
Db 300 CGCATATCTGGACAGTAGAAGGGCTTCATCATATCAATATGCAACGTACAAAGAAATA 359
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 360
Db 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAAGACAAACTATCTCACA 419
QY 361 CATCGACAAACCAATCAATCATAGATGTGTCTTCTGAGTCCGTCTCATGGAATTGAACATA 420
Db 420 CATCGACAAACCAATCAATCATAGATGTGTCTTCTGAGTCCGTCTCATGGAATTGAACATA 479
QY 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATTAATGTGGGGATT 480
Db 480 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATTAATGTGGGGATT 539
QY 481 GACTTCAACTGGGAATACCTTCTTTCGAAGCATCAGCATAGCAAACTTGTAAACCGAGAC 540
Db 540 GACTTCAACTGGGAATACCTTCTTTCGAAGCATCAGCATAGCAAACTTGTAAACCGAGAC 599
QY 541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACTATAGATGGT 600
Db 600 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACTATAGATGGT 659
QY 601 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGACAGATCAGTGGGCTGATGACCAAG 660
Db 660 GTAAACCCGGAGTGACCAAGGATTGTACACCTGTGACAGATCAGTGGGCTGATGACCAAG 719
QY 661 AAGAACAGCACATTTGTGAGGTCCATGAAAG-----GACAAACTCACAATGC 711
Db 720 AAGAACAGCACATTTGTGAGGTCCATGAAAGGGCCCGGGCGACAAACTCACAATGC 779
QY 712 CCACCGTCCCAAGCACCTGAACTCTCTGGGGGACCGTCACTCTTCTTCTCCCCCAAAA 771
Db 780 CCACCGTCCCAAGCACCTGAACTCTCTGGGGGACCGTCACTCTTCTTCTCCCCCAAAA 839
QY 772 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGACGTG 831
Db 840 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGACGTG 899
QY 832 AGCCACGAGACCTGAGGTCAAGTTCAACTGCTAGTGGAGCGGCTGAGGTGATAT 891
Db 900 AGCCACGAGACCTGAGGTCAAGTTCAACTGCTAGTGGAGCGGCTGAGGTGATAT 959
QY 892 GCACAGACAAAGCCCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCTCCTC 951
Db 960 GCACAGACAAAGCCCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCTCCTC 1019
QY 952 ACCGTCTGACACGAGTCTGCTGAATGGCAAGGAGTCAAGTGAAGGTCTCCAAACAA 1011
Db 1020 ACCGTCTGACACGAGTCTGCTGAATGGCAAGGAGTCAAGTGAAGGTCTCCAAACAA 1079
QY 1012 GCCTCCAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGCCCGGAGAACCA 1071
Db 1080 GCCTCCAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGCCCGGAGAACCA 1139
QY 1072 CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGAGCTGACC 1131
Db 1140 CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCCAGGTGAGCTGACC 1199
QY 1132 TGCTGTGTAAGGGCTTCTATCCAGCGACATGCGCGTGGAGTGGAGAGCAATGGGGAG 1191
Db 1200 TGCTGTGTAAGGGCTTCTATCCAGCGACATGCGCGTGGAGTGGAGAGCAATGGGGAG 1259
QY 1192 CCGGAGAACAACTACAAGACCGCTCCCGTGTGAGTCCGAGCGGCTCTTCTCTC 1251
Db 1260 CCGGAGAACAACTACAAGACCGCTCCCGTGTGAGTCCGAGCGGCTCTTCTCTC 1319
```

```
QY 1252 TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCC 1311
Db 1320 TATAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCC 1379
QY 1312 GTGATGATGAGGCTCTGCACAACTACACGACGAAGAGCCTCTCCCTGTCTCCGGGT 1371
Db 1380 GTGATGATGAGGCTCTGCACAACTACACGACGAAGAGCCTCTCCCTGTCTCCGGGT 1439
QY 1372 AAATGA 1377
Db 1440 AAATGA 1445

RESULT 3
AX056747
LOCUS AX056747 1444 bp DNA linear PAT 17-JAN-2001
DEFINITION Sequence 13 from Patent WO0075319.
ACCESSION AX056747
VERSION AX056747.1 GI:12309726
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.
TITLE Modified chimeric polypeptides with improved pharmacokinetic
JOURNAL properties
Patent: WO 0075319-A 13 14-DEC-2000;
REGENERON PHARMACEUTICALS, INC. (US)
FEATURES
source
1..1444
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
69..1436
/note="unnamed protein product"
/codon_start=1
/protein_id="CAC22378.1"
/db_xref="GI:12309727"
/translation="MVSVDYDGLVLLALLSLLLTGSSSGRPFVVMYSSEIPELIHMT
EGRELIVPCRVTPNITVTLKPLDPLIDPKRIIWDNRKFIISNATYKBIIGLTC
EATVNGHLYKNTYLTHRTNTIIDIQLPKRSLLELVGEKLVLNCTVMAEFSVTFD
WYPGKAERKQVRRSQOHTTIIHNSQHDLSGYVCKNANGIQRFRST
EVIHENGPDKTHTPCPAPPELLGGPSVFLPPKPKDLMISRTPEVTCVVDVSH
EDPEKFNWYVDGVEVHNAKTQREQVNSTYRVSVLTVLHQDWLNGKEYKCKVSNK
ALPAPIKTSISKAGQPRFQVTLPSRDELTKNQVSLTCLVKGFIPSDIAVESWEN
GQPENNYKTTTPPVLDSGSPFLYSKLTVDKSRWQQGNVFCGSVMHEALHNHYTKSL
LSPGK"
ORIGIN
Query Match 76.2%; Score 1049.2; DB 6; Length 1444;
Best Local Similarity 86.7%; Pred. No. 1.4e-233;
Matches 1201; Conservative 0; Mismatches 158; Indels 27; Gaps 3;
QY 1 ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60
Db 69 ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 128
QY 61 ACAGGATCTAGTCCGGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC 120
Db 129 ACAGGATCTAGTCCGGA-----GGTAGACCTTTCTGTAGAGATGTACAGTGAATC 179
QY 121 CCGGAATATTACATGATGATGAGGAAGGGAGCTCGTCAATCCCTCGCGGTTACGTCA 180
Db 180 CCGGAATATTACATGATGATGAGGAAGGGAGCTCGTCAATCCCTCGCGGTTACGTCA 239
QY 181 CCTAACATCACTGTTACTTTTAAAGAGTTTCCACTTGCACACTTTGATCCCTGATGAAAA 240
Db 240 CCTAACATCACTGTTACTTTTAAAGAGTTTCCACTTGCACACTTTGATCCCTGATGAAAA 299
QY 241 CGCATATCTGGGACAGTAGAAGGGCTTCAATCATATCAATATGCAACGTACAAAGAAATA 300
```

Db 300 CGCATAATCTGGGACAGTAGAAAGGGCTTCATCATCAATGCAACGTACAAAGAAATA 359  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 360  
Db 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 419  
Qy 361 CATGCACAAACCAATACAAATCATAGATGTGGTCTCTGAGTCCGTCTCATGGAATTGAACCTA 420  
Db 420 CATGCACAAACCAATACAAATCATAGATCATAGATATCAGCTGTGGCCAGGAAGTCCGTGGAGCTG 479  
Qy 421 TCTGTGTGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATTT 480  
Db 480 CTGGTAGGGGAGAAGCTGCTCCTCACTGCACCGTGTGGCTGAGTTTAACTCAGGTCTC 539  
Qy 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATTAAGAACTTGTAAACCGAGAC 540  
Db 540 ACCTTTGACTGGGACTACCCAGGAAGCAGGACGAGCGGGTAAAGTGGTCCCGAGCGA 599  
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACCTATAGATGGT 600  
Db 600 CGTCTCCCAACAGACCCACACAG-----AACTCTCCAGCATCCTGACCATCCACAAC 650  
Qy 601 GTAAACCCGGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Db 651 GTCAGCCAGCAGACCTGGCTCGTATGTGTGCAAGGCCAACAACGGCATCCAGCGATTT 710  
Qy 661 AAGAACAGCACATTTGTGAGGTCATGAATA-----GGACAAACTCACAATGC 711  
Db 711 CGGGAGACACCGAGGTCATTTGTGCATGAATAATGGCCGGCGACAAACTCACAATGC 770  
Qy 712 CCACCGTCCAGACCTGAACTCTGGGGGACCGTCACTGCTCTTCTTCCCGCCCAAA 771  
Db 771 CCACCGTCCAGACCTGAACTCTGGGGGACCGTCACTGCTCTTCTTCCCGCCCAAA 830  
Qy 772 CCCAAGGACACCCCTCATGATCTCCGGGACCCCTCAGAGTCAATGCGTGGTGGAGCGTG 831  
Db 831 CCCAAGGACACCCCTCATGATCTCCGGGACCCCTCAGAGTCAATGCGTGGTGGAGCGTG 890  
Qy 832 AGCCACGAGAACCTGAGGTCAGTTCACTGTGTAAGTGAGACGGGCTGGAGGTCATTAAT 891  
Db 891 AGCCACGAGAACCCCTGAGGTCAGTTCACTGTGTAAGTGAGACGGGCTGGAGGTCATTAAT 950  
Qy 892 GCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTCAAGCTCTC 951  
Db 951 GCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGGTGGTCAAGCTCTC 1010  
Qy 952 ACCGTCTCTGACCAAGGACTGGCTGAATGGCAAGGAGTCAAGTGCAAGGTCCTCCAAACAA 1011  
Db 1011 ACCGTCTCTGACCAAGGACTGGCTGAATGGCAAGGAGTCAAGTGCAAGGTCCTCCAAACAA 1070  
Qy 1012 GCGTCCGAGCCCGCATCGAAGAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1071  
Db 1071 GCGTCCGAGCCCGCATCGAAGAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1130  
Qy 1072 CAGGTGTACACCTGCGCCCATCCCGGATCAGCTGACCAAGAACCCAGTCAAGCTGAC 1131  
Db 1131 CAGGTGTACACCTGCGCCCATCCCGGATCAGCTGACCAAGAACCCAGTCAAGCTGAC 1190  
Qy 1132 TGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAG 1191  
Db 1191 TGCTGTGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAG 1250  
Qy 1192 CCGGAGAACACTACAGACCCGCTCCCGTGTGGACTCCGAGCGGCTCTTCTTCTCTC 1251  
Db 1251 CCGGAGAACACTACAGACCCGCTCCCGTGTGGACTCCGAGCGGCTCTTCTTCTCTC 1310  
Qy 1252 TACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGGAAACGCTTCTCATGTCTCC 1311  
Db 1311 TATAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGAGGGGAAACGCTTCTCATGTCTCC 1370  
Qy 1312 GTGATGCAATGAGGCTCTGCAACCAACTACACGAGAGAGCCCTCTCCCTGTCTCCGGGT 1371  
Db 1371 GTGATGCAATGAGGCTCTGCAACCAACTACACGAGAGAGCCCTCTCCCTGTCTCCGGGT 1430

Qy 1372 AAATGA 1377  
Db 1431 AAATGA 1436

RESULT 4  
AX056739 LOCUS 1359 bp DNA linear PAT 17-JAN-2001  
DEFINITION Sequence 5 from Patent WO0075319.  
ACCESSION AX056739  
VERSION AX056739.1 GI:12309718  
KEYWORDS Homo sapiens (human)  
SOURCE  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1  
Papadopoulos, N.J., Davis, S. and Yancopoulos, G.D.  
Modified chimeric polypeptides with improved pharmacokinetic  
properties  
Patent: WO 0075319-A 5 14-DEC-2000;  
REGENERON PHARMACEUTICALS, INC. (US)  
FEATURES  
Location/Qualifiers  
1..1359  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
1..1359  
/note="unnamed protein product"  
/codon\_start=1  
/protein\_id="CAC22374.1"  
/db\_xref="GI:12309719"

CDS  
1..1359  
/translation="MVSYNDTVLLCALLSLTSSSGRPFVEMYSEIPELIHMT  
EGRELVIPCRVTSFNITVTLKFPDLDTIPDGKRIIWDNRKGIISNATYKEIGLLTC  
EATVNGHLKYNTVLTHTQNTIIDVOISTPRVKLLRGHTLVNCTATTPLNTRVQMT  
WSYPRDEIDQSNSHANIFYSVLITIDMKNQDKGLYTCRVRSRSPFKSVNTSVHIVDKAG  
PGBPKSCDKHTCTPCPCAPPELLGLGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDP  
EVFNMTVDGVEVHNATKPREQSYNSTYKRVSVLTVLHQDLNGLKREYCKCKSVNKALP  
APIETKISAKGQPRFPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGQP  
ENRYKPTTPPVLDSGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP  
GK"

ORIGIN  
Query Match 75.5%; Score 1039; DB 6; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 3.4e-231;  
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;  
Qy 1 ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60  
Db 1 ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTC 60  
Qy 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCCGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC 111  
Qy 121 CCGAATATTATACATGACTGTAAGGAGGAGCTCGTCATTCCTCCCGGGTTACGTCA 180  
Db 112 CCGAATATTATACATGACTGTAAGGAGGAGCTCGTCATTCCTCCCGGGTTACGTCA 171  
Qy 181 CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGTAGGAAAA 240  
Db 172 CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGTAGGAAAA 231  
Qy 241 CGCATAAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGTCAAAAGAAATA 300  
Db 232 CGCATAAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGTCAAAAGAAATA 291  
Qy 301 GGGCTTCTGACCTGTGAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 360  
Db 292 GGGCTTCTGACCTGTGAGCAACAGTCAATGGGCATTTGTATAGACAAACTATCTCACA 351  
Qy 361 CATGCACAAACCAATACAAATCATAGATGTGGTCTGAGTCCGTCTCATGGAATTGAACCTA 420









QY	892	GCCAAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCTCAGCGTCTC	951
Db	1219	GCCAAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCAGTACCGTGTGGTCTCAGCGTCTC	1278
QY	952	ACCGTCTCTGACACAGGAGTGGCTGAATGGCAAGAGTACAAGTGCAGAGTCTTCCAAACAA	1011
Db	1279	ACCGTCTCTGACACAGGAGTGGCTGAATGGCAAGAGTACAAGTGCAGAGTCTTCCAAACAA	1338
QY	1012	GCCCTCCAGAGCCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCA	1071
Db	1339	GCCCTCCAGAGCCCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCA	1398
QY	1072	CAGGTGTACACCTCCGCCCATCCCGGATGAGCTGACCAAGNACCAGTCTGAGCTGACC	1131
Db	1399	CAGGTGTACACCTCCGCCCATCCCGGATGAGCTGACCAAGNACCAGTCTGAGCTGACC	1458
QY	1132	TGCTGGTCAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAG	1191
Db	1459	TGCTGGTCAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAG	1518
QY	1192	CGGAGAACAACTACAAGACACGCTCCCGTGTGGACTCGACGGCTCTTCTTCTC	1251
Db	1519	CGGAGAACAACTACAAGACACGCTCCCGTGTGGACTCGACGGCTCTTCTTCTC	1578
QY	1252	TACAGCAAGCTCACCGTGGACAGAGCAGTGGGACGAGGGGAGCGTCTTCTCATGCTCC	1311
Db	1579	TACAGCAAGCTCACCGTGGACAGAGCAGTGGGACGAGGGGAGCGTCTTCTCATGCTCC	1638
QY	1312	GTGATGATAGGCTCTGACAAACCACTACACGACGAGAGCGCTCTCCCTGTCTCCGGGT	1371
Db	1639	GTGATGATAGGCTCTGACAAACCACTACACGACGAGAGCGCTCTCCCTGTCTCCGGGT	1698
QY	1372	AAATGA 1377	
Db	1699	AAATGA 1704	
RESULT 8			
AX056735			
LOCUS			
DEFINITION			
Sequence 1 from Patent WO0075319.			
ACCESSION			
AX056735			
VERSION			
AX056735.1 GI:12309714			
KEYWORDS			
SOURCE			
Homo sapiens (human)			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE			
Papadopoulos,N.J., Davis,S. and Yancopoulos,G.D.			
AUTHORS			
Modified chimeric polypeptides with improved pharmacokinetic			
properties			
JOURNAL			
Patent: WO 0075319-A 1 14-DEC-2000;			
REGENERON PHARMACEUTICALS, INC. (US)			
FEATURES			
source			
1..1704			
/organism="Homo sapiens"			
/mol_type="unassigned DNA"			
/db_xref="taxon:9606"			
1..1704			
/note="unnamed protein product"			
/codon_start=1			
/protein_id="CAC22372.1"			
/db_xref="GI:12309715"			
/translation="WVSVDVGLLCALLSLTSSGSKLDPSELKGTQHIWQ			
AGTILHLCGEAAHKSLEPMVSKESERLSITKACGRNGKQFCSTILTNTAQANT			
GFYCKYLAIVPSKKETESAIYIFSDTGRPFVMEYSEPIIIMHTEGRELVIPICR			
TSPNITVLKFPFLDLPDGRKIIWDSRKGFIISNATYKIEIGLLTCEATVNGHLYKT			
NLYRHQNTNIDYQISFVPEVRLKRLHGLVINCTATTPNLNTRVQMTWSYFDEKNKA			
SVRRIDQSNHANI FSVLTIDKQNDKGLYTCVRSGSPFSKSVNTSVH IYDKAGP			
GEPSCKDHTCPCPAPELLGSPVFLFPKPKDTLMI SRTPEVTCVVDVSHEDPE			
VKFNWYVDGVEVHNAKTKPREQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA			
CDS			
Query Match			
Beet Local Similarity 71.2%; Score 980.8; DB 6; Length 1704;			
Matches 1131; Predictive 85.3%; Pred. No. 1.2e-217; Indels 33; Gaps 2;			
Mismatches 0; Mismatches 162; Indels 33; Gaps 2;			
QY	79	AGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATCCCGGAAATTTATACACATG	138
Db	385	AGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATTTATACACATG	444
QY	139	ACTGAAGGAGGAGTCTGTCATTCCTGCGGGTACGTCACCTAACATCAGTCTTACT	198
Db	445	ACTGAAGGAGGAGTCTGTCATTCCTGCGGGTACGTCACCTAACATCAGTCTTACT	504
QY	199	TTAAAAAGTTTCCACCTTGACACTTTTCATCCCTGATGAAAAACGATAATCTGGGACAGT	258
Db	505	TTAAAAAGTTTCCACCTTGACACTTTTCATCCCTGATGAAAAACGATAATCTGGGACAGT	564
QY	259	AGAAAGGCTTCATCATATCAAAATGCAACGCTACAAAGAAATAGGGCTTCTGACCTGTGAA	318
Db	565	AGAAAGGCTTCATCATATCAAAATGCAACGCTACAAAGAAATAGGGCTTCTGACCTGTGAA	624
QY	319	GCAACAGTCAATGGGCAATTTGTATAGACAAAATATCTCTCACATCGACAAAACCAATACA	378
Db	625	GCAACAGTCAATGGGCAATTTGTATAGACAAAATATCTCTCACATCGACAAAACCAATACA	684
QY	379	ATCATAGATGTGGTTCGTGAGTCCGTCTCATGGAATGAACTATCTGTGGGAGAAAGCTT	438
Db	685	ATCATAGATGTGGTTCGTGAGTCCGTCTCATGGAATGAACTATCTGTGGGAGAAAGCTT	744
QY	439	GTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGGAATTGACTTCAACTGGGAATAC	498
Db	745	GTCTTAAATTTGACAGCAAGAACTGAACTAAATGTGGGGAATTGACTTCAACTGGGAATAC	804
QY	499	CTTCTTTCGAGAGCATCAGCATAGAAACTTTGTAACCGGACCTTAAACCCAGGAGTCTGGG	558
Db	805	CTTCTTTCGAGAGCATCAGCATAGAAACTTTGTAACCGGACCTTAAACCCAGGAGTCTGGG	858
QY	559	AGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGTGTAAACCCGAGGTGACAA	618
Db	859	AGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGTGTAAACCCGAGGTGACAA	918
QY	619	GGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAGAGAAACAGCATTTTGTGTC	678
Db	919	GGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAGAGAAACAGCATTTTGTGTC	978
QY	679	AGGTTCATGAAA-----GGACAAAACCTCACATGC	711
Db	979	CATATATATGATAAAGCAGCGCCGCGGAGCCCAAAATCTTTGTGACAAAACCTCACATGC	1038
QY	712	CCACCGTCCGACACCTGAACTCCCTGGGGGAGCCGTCAGTCTTCTTCCCCCAAAA	771
Db	1039	CCACCGTCCGACACCTGAACTCCCTGGGGGAGCCGTCAGTCTTCTTCCCCCAAAA	1098
QY	772	CCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGTGGAGCGTG	831
Db	1099	CCAAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGTGGAGCGTG	1158
QY	832	AGCCACGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGAGGTGCAAT	891
Db	1159	AGCCACGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGTGGAGGTGCAAT	1218
QY	892	GCCAAAGCAAGCGCGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTGTGGTGGTGGTGGT	951
Db	1219	GCCAAAGCAAGCGCGGAGGAGGAGCAGTACAACAGCAGCTACCGTGTGGTGTGGTGGTGGTGGT	1278
QY	952	ACCGTCTCTGACACGAGGACTCGCTGAATGGCAAGAGTACAAGTGCAGAGTCTTCCAAACAA	1011
Db	1279	ACCGTCTCTGACACGAGGACTCGCTGAATGGCAAGAGTACAAGTGCAGAGTCTTCCAAACAA	1338

PIEKTISKAGOPREPOVYTLPPSRDELTKNOVSLTCLVKGFVPSDIAVVEWSNGOPE  
NNYKTPPVLDSDSGSPFLYSKLIYDKSRWQGNVFSVHMHEALHNHYTKSLSLSPG  
K"



Db	1550	TGCAATAATGCCAACCAAGCCGGGAGGACAGTACAAACAGCACGTACCGGGTGGTCA	1609
Qy	944	GCGTCTTCACCGTCTCTGCACACAGGACTGGCTGAATGGCAAGGAGTCAACAGTGCACAGGTCT	1003
Db	1610	GCGTCTCTACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTCAACAGTGCACAGGTCT	1669
Qy	1004	CCAAACAAAGCCCTCCACGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC	1063
Db	1670	CCAAACAAAGCCCTCCACGCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCC	1729
Qy	1064	GAGAACACACAGGTGTACACCGTGCCTCCCATCCCGGGATGAGCTGACCAAGAACACAGGTCA	1123
Db	1730	GAGAACACACAGGTGTACACCGTGCCTCCCATCCCGGGATGAGCTGACCAAGAACACAGGTCA	1789
Qy	1124	GCCTGACCTGCCTGGTCAAAAGGCTTCTATCCACAGCGACATCGCGTGGAGTGGGAGAGCA	1183
Db	1790	GCCTGACCTGCCTGGTCAAAAGGCTTCTATCCACAGCGACATCGCGTGGAGTGGGAGAGCA	1849
Qy	1184	ATGGCAGCGGAGAACAACTACAAGACCAACGCTCCCGTGTCTGGACTCCGACGGCTCCT	1243
Db	1850	ATGGCAGCGGAGAACAACTACAAGACCAACGCTCCCGTGTCTGGACTCCGACGGCTCCT	1909
Qy	1244	TCCTTCCTCTACAGCAAGCTCACCGTGCACAAAGACAGGTGGCAGCGGGGAAAGCTTCTCT	1303
Db	1910	TCCTTCCTCTACAGCAAGCTCACCGTGCACAAAGACAGGTGGCAGCGGGGAAAGCTTCTCT	1969
Qy	1304	CATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGACAGAGAGGCTCTCCCTGT	1363
Db	1970	CATGCTCCGTGATGCATGAGGCTCTGCACAAACCACTACACGACAGAGAGGCTCTCCCTGT	2029
Qy	1364	CTCCGGGTAAATGA	1377
Db	2030	CTCCGGGTAAATGA	2043

```

RESULT 11
AR380678 LOCUS AR380678 705 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1223 from patent US 6607879.
ACCESSION AR380678
VERSION AR380678.1 GI:40088312
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 705)
AUTHORS Cocks/B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological
response gene expression
JOURNAL Patent: US 6607879-A 1223 19-AUG-2003;
FEATURES
source Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 49.7%; Score 684; DB 6; Length 705;
Best Local Similarity 100.0%; Pred. NO. 1.6e-148;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 694 GACAAACTCACATGCCACCGTGGCCAGCACCTGAATCTCTGGGGGACCGTCAGTC 753
|||
Db 5 GACAAAACTCACATGCCACCGTGGCCAGCACCTGAATCTCTGGGGGACCGTCAGTC 64
|||
Qy 754 TTCCTCTTCCCCCAAAACCCAAGACACCTCATGATCTCCGGGACCCCTGAGGTCACA 813
|||
Db 65 TTCCTCTTCCCCCAAAACCCAAGACACCTCATGATCTCCGGGACCCCTGAGGTCACA 124
|||
Qy 814 TGC GTGTGTGTGACGTGAGCCAGAACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
|||
Db 125 TGC GTGTGTGTGACGTGAGCCAGAACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 184
|||

```

QY	874	GGCGTGAGGTGCATAATGCGAAGCAAAAGCCGGGAGGAGCAGTACAACAGCACGTAC	933
Db	185	GGCGTGAGGTGCATAATGCGAAGCAAAAGCCGGGAGGAGCAGTACAACAGCACGTAC	244
QY	934	CGTGTGCTACGCTCCTCAGGTCCTGCACCGAGCTCGCTGAATGGCAAGGAGTACAAG	993
Db	245	CGTGTGCTACGCTCCTCAGGTCCTGCACCGAGCTCGCTGAATGGCAAGGAGTACAAG	304
QY	994	TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA	1053
Db	305	TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA	364
QY	1054	GGGAGAGCCCGAGAACACAGAGGTGTACACCTTGCCCCCATCCCGGAGTAGCTGACCAAG	1113
Db	365	GGGAGAGCCCGAGAACACAGAGGTGTACACCTTGCCCCCATCCCGGAGTAGCTGACCAAG	424
QY	1114	AACAGAGTCAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG	1173
Db	425	AACAGAGTCAGCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG	484
QY	1174	TGGAGAGCAATGGGACCGCGAGAACAACTACAAGACCAAGCTCCCGTGTGGACTCC	1233
Db	485	TGGAGAGCAATGGGACCGCGAGAACAACTACAAGACCAAGCTCCCGTGTGGACTCC	544
QY	1234	GACGGCTCCTTCTTCCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG	1293
Db	545	GACGGCTCCTTCTTCCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG	604
QY	1294	AACGCTCTTCATGCTCCGCTGATGCATGAGGCTCTGCAACCACTACACGAGAAGAGC	1353
Db	605	AACGCTCTTCATGCTCCGCTGATGCATGAGGCTCTGCAACCACTACACGAGAAGAGC	664
QY	1354	CTCTCCCTGTCTCCGGTAAATGA	1377
Db	665	CTCTCCCTGTCTCCGGTAAATGA	688
RESULT 12			
AX556168		762 bp	DNA
LOCUS	AX556168	Sequence 17 from Patent WO0238766.	linear
DEFINITION	AX556168		PAT 27-NOV-2002
ACCESSION	AX556168.1		
VERSION	AX556168.1	GI:25899545	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Gross, J. A., Xu, W., Henne, R. M. and Grant, F. J.		
TITLE	Human tumor necrosis factor receptor		
JOURNAL	Patent: WO 0238766-A 17 16-MAY-2002;		
FEATURES	ZymoGenetics, Inc. (US)		
source	Location/Qualifiers		
	1. .762		
	/note="unnamed protein product"		
	/codon_start=1		
	/protein_id="CAD58267.1"		
	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
CDS	7. .762		
	/translation="MKHLWFLLLVAAPRWLSEPKSCDKTHTCPCPAPELVGGPSV		
	FLFPKPKDILMSIRPEVTCVVVDVSHEDPEVKFNWYDGVENHNAKTKPREQNS		
	TYRVSQVLTVLHQDMLNGKEYICKVSNKALPAIEKTI SKAGQPREPQVYITLPPGRD		
	ELTGNQSLTCLVKIGFVPSDYSWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK		
	SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK"		
ORIGIN			





PC C12N15/09, A61K9/48, A61K38/00, A61K39/395, A61K48/00, A61P1/04, PC  
A61P1/15,  
PC A61P3/10, A61P7/06, A61P9/02, A61P11/02, A61P11/06, A61P17/00, PC  
A61P17/06,  
PC A61P19/02, A61P21/02, A61P21/04, A61P25/00, A61P35/00, A61P37/02,  
PC A61P37/06,  
PC C07K14/705, C07K16/46, C07K19/00, C12N5/10, C12N15/00, C12N5/00, PC  
A61K37/02  
CC Description of Sequence: Recombinant Polynucleotide FH Key  
FT CDS Location/Qualifiers  
source 1. .1019  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 49.7%; Score 684; DB 6; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 1.7e-148; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0;  
Qy 694 GACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTC 753  
Db 328 GACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTC 387  
Qy 754 TTCCTCTTCCCTCCCAAAACCCAGGACACCTCTCATGATCTCCCGGACCCCTGAGGTACACA 813  
Db 388 TTCCTCTTCCCTCCCAAAACCCAGGACACCTCTCATGATCTCCCGGACCCCTGAGGTACACA 447  
Qy 814 TGCCTGTGTGGTGGACGTCAGCAGCACCAAGACCTCTGAGGTCAAGTTCAACTGCTAGTGGAC 873  
Db 448 TGCCTGTGTGGTGGACGTCAGCAGCACCAAGACCTCTGAGGTCAAGTTCAACTGCTAGTGGAC 507  
Qy 874 GGCCTGGAGGTGCATAATGCCAAGACCAAGCCGCGGAGGAGCAGTACAAACAGCACGTCAC 933  
Db 508 GGCCTGGAGGTGCATAATGCCAAGACCAAGCCGCGGAGGAGCAGTACAAACAGCACGTCAC 567  
Qy 934 CGTGTGTGACGGTCTCAGCGTCTTGCAACAGGACTGGCTGTAATGGCAAGGATACAAAG 993  
Db 568 CGTGTGTGACGGTCTCAGCGTCTTGCAACAGGACTGGCTGTAATGGCAAGGATACAAAG 627  
Qy 994 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCTCCAGAGAAACCACTCTCCAAAGCCAAA 1053  
Db 628 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCTCCAGAGAAACCACTCTCCAAAGCCAAA 687  
Qy 1054 GGGCAGCCCCGAGAACACAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGACCAAG 1113  
Db 688 GGGCAGCCCCGAGAACACAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGACCAAG 747  
Qy 1114 AACGAGTCAAGCTGACCTGCTGTTCAAGGCTTCTATCCAGGACATCGCCGTGGAG 1173  
Db 748 AACGAGTCAAGCTGACCTGCTGTTCAAGGCTTCTATCCAGGACATCGCCGTGGAG 807  
Qy 1174 TGGGAGAGCAATGGGACGCGGAGAACAACTACAGACACGCTCCCGTCTGCACTCC 1233  
Db 808 TGGGAGAGCAATGGGACGCGGAGAACAACTACAGACACGCTCCCGTCTGCACTCC 867  
Qy 1234 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 1293  
Db 868 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 927  
Qy 1294 AACGCTCTTCTCATGTCTCGGTGATGATGAGGCTCTGCAACCACTACACGAGAGAGC 1353  
Db 928 AACGCTCTTCTCATGTCTCGGTGATGATGAGGCTCTGCAACCACTACACGAGAGAGC 987  
Qy 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377  
Db 988 CTCTCCCTGTCTCCGGGTAAATGA 1011

RESULT 15  
AR275187

LOCUS AR275187 1019 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 1 from patent US 6506891.  
ACCESSION AR275187  
VERSION AR275187.1 GI:29708174  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1019)  
AUTHORS Tao, W., Wong, S., Hickey, W. F., Hamang, J. P. and Baetge, E. E.  
TITLE Cell surface molecule-induced macrophage activation  
JOURNAL Patent: US 6506891-A 1 14-JAN-2003;  
FEATURES  
source 1. .1019  
/organism="unknown"  
/mol\_type="genomic DNA"  
ORIGIN  
Query Match 49.7%; Score 684; DB 6; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 1.7e-148; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0;  
Qy 694 GACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTC 753  
Db 328 GACAAAACCTCACACATGCCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAAGTC 387  
Qy 754 TTCCTCTTCCCTCCCAAAACCCAGGACACCTCTCATGATCTCCCGGACCCCTGAGGTACACA 813  
Db 388 TTCCTCTTCCCTCCCAAAACCCAGGACACCTCTCATGATCTCCCGGACCCCTGAGGTACACA 447  
Qy 814 TGCCTGTGTGGTGGACGTCAGCAGCACCAAGACCTCTGAGGTCAAGTTCAACTGCTAGTGGAC 873  
Db 448 TGCCTGTGTGGTGGACGTCAGCAGCACCAAGACCTCTGAGGTCAAGTTCAACTGCTAGTGGAC 507  
Qy 874 GGCCTGGAGGTGCATAATGCCAAGACCAAGCCGCGGAGGAGCAGTACAAACAGCACGTCAC 933  
Db 508 GGCCTGGAGGTGCATAATGCCAAGACCAAGCCGCGGAGGAGCAGTACAAACAGCACGTCAC 567  
Qy 934 CGTGTGTGACGGTCTCAGCGTCTTGCAACAGGACTGGCTGTAATGGCAAGGATACAAAG 993  
Db 568 CGTGTGTGACGGTCTCAGCGTCTTGCAACAGGACTGGCTGTAATGGCAAGGATACAAAG 627  
Qy 994 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCTCCAGAGAAACCACTCTCCAAAGCCAAA 1053  
Db 628 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCCTCCAGAGAAACCACTCTCCAAAGCCAAA 687  
Qy 1054 GGGCAGCCCCGAGAACACAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGACCAAG 1113  
Db 688 GGGCAGCCCCGAGAACACAGGTGTACACCTTGCCCCCATCCCGGGATGAGCTGACCAAG 747  
Qy 1114 AACGAGTCAAGCTGACCTGCTGTTCAAGGCTTCTATCCAGGACATCGCCGTGGAG 1173  
Db 748 AACGAGTCAAGCTGACCTGCTGTTCAAGGCTTCTATCCAGGACATCGCCGTGGAG 807  
Qy 1174 TGGGAGAGCAATGGGACGCGGAGAACAACTACAGACACGCTCCCGTCTGCACTCC 1233  
Db 808 TGGGAGAGCAATGGGACGCGGAGAACAACTACAGACACGCTCCCGTCTGCACTCC 867  
Qy 1234 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 1293  
Db 868 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGG 927  
Qy 1294 AACGCTCTTCTCATGTCTCGGTGATGATGAGGCTCTGCAACCACTACACGAGAGAGC 1353  
Db 928 AACGCTCTTCTCATGTCTCGGTGATGATGAGGCTCTGCAACCACTACACGAGAGAGC 987  
Qy 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377  
Db 988 CTCTCCCTGTCTCCGGGTAAATGA 1011

Search completed: August 27, 2005, 05:29:22  
Job time : 6129.4 secs

---

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 20:54:45 ; Search time 787.087 Seconds  
(without alignments)  
10356.518 Million cell updates/sec

Title: US-10-009-852-15

Perfect score: 1377

Sequence: 1 atggtcagctactgggacac.....cctgtctccgggtaaatga 1377

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N\_Geneseq\_16Dec04:\*  
1: Geneseqn1980a:\*  
2: Geneseqn1990a:\*  
3: Geneseqn2000a:\*  
4: Geneseqn2001a:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1377	100.0	1377	5	AA91076
2	1377	100.0	1377	6	ABQ74610 Modified
3	1328.4	96.5	1453	5	AA91074
4	1328.4	96.5	1453	6	ABQ74608 Modified
5	1049.2	76.2	1444	5	AA91075
6	1049.2	76.2	1444	6	ABQ74609 Modified
7	1039	75.5	1359	5	AA91071
8	1039	75.5	1359	6	ABQ74605 Mutation
9	1032.4	75.0	1389	5	AA91072
10	1032.4	75.0	1389	6	ABQ74606 Mutation
11	987.4	71.7	1674	5	AA91070
12	987.4	71.7	1674	6	ABQ74604 Mutation
13	982.4	71.3	1704	5	AA91073
14	982.4	71.3	1704	6	ABQ74607 Mutation
15	980.8	71.2	1704	5	AA91077
16	980.8	71.2	1704	6	ABQ74603 Ftl1(1-3)
17	687.8	49.9	1290	10	AA156122 Plasmid p
18	687.8	49.9	1290	12	AD010510 Kb/EP0/Ig
19	687.8	49.9	1299	10	AA156123 Plasmid p
20	687.8	49.9	1299	12	AD010512 EPO/IgG1

21	687.2	49.9	1383	6	AA167766	AA167766 Human Ryk
22	687.2	49.9	1389	10	ADC98597	ADC98597 Human ang
23	687.2	49.9	1470	10	ADC98595	ADC98595 Human ang
24	687.2	49.9	1767	10	ADC98593	ADC98593 Human ang
25	687.2	49.9	1947	10	ADC98589	ADC98589 Human ang
26	687.2	49.9	1998	10	ADC98591	ADC98591 Human ang
27	687.2	49.9	2094	10	ADC98613	ADC98613 Human ang
28	687.2	49.9	2118	10	ADC98587	ADC98587 Human ang
29	687.2	49.9	2181	10	ADC98585	ADC98585 Human ang
30	687.2	49.9	2652	10	ADC98567	ADC98567 Human ang
31	686	49.8	2043	2	AAQ55340	AAQ55340 tICAM(453
32	685.2	49.8	798	10	AA156121	AA156121 Plasmid p
33	685.2	49.8	798	12	AD010508	AD010508 Kb signal
34	685	49.7	6097	5	AAF57869	AAF57869 OPG-Fc co
35	684	49.7	705	11	AD131897	AD131897 Human CDN
36	684	49.7	705	12	ADL46173	ADL46173 Human imm
37	684	49.7	762	6	ABN89435	ABN89435 Human imm
38	684	49.7	762	10	AA53735	AA53735 Human wil
39	684	49.7	762	10	AA53755	AA53755 Human mod
40	684	49.7	762	10	AA53760	AA53760 Human mod
41	684	49.7	993	12	ADM68909	ADM68909 Human Igg
42	684	49.7	1002	12	ADL22760	ADL22760 Human ant
43	684	49.7	1002	12	ADN97484	ADN97484 Artificial
44	684	49.7	1019	3	AA53126	AA53126 Human TR-
45	684	49.7	1182	2	AAV34430	AAV34430 Antigenic

## ALIGNMENTS

RESULT 1

AAA91076

ID AAA91076 standard; DNA; 1377 BP.

XX

AC AAA91076;

XX

DT 05-APR-2001 (first entry)

XX

DE Ftl1 receptor fusion protein VEGFR1R2-FcDeltaC2 (a) coding sequence.

XX

KW Ftl1 receptor; fusion protein; chimeric protein; pharmacokinetic;

KW plasma leakage; vascular permeability; Igg Fc region; ss.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT CDS 1..1377

FT /\*tag= a

FT /product= "VEGFR1R2-FcDeltaC2(a)"

XX

PN WO200075319-A1.

XX

PD 14-DEC-2000.

XX

PF 23-MAY-2000; 2000WO-US014142.

XX

PR 08-JUN-1999; 99US-0138133P.

XX

PA (REGE-) REGENERON PHARM INC.

XX

PI Papadopoulos NJ, Davis S, Yancopoulos GD;

XX

DR WPI; 2001-071076/08.

XX

DR P-PSDB; AA97596.

XX

PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,

PT and its fragments, useful for diagnosis, evaluation, and treatment of

PT diseases associated with the gene expression and for producing model

XX

PS Claim 9; Fig 24; 159pp; English.

CC This sequence encodes a fusion protein of the invention between the Ftl1

receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Flk1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular permeability in a mammal

```

Q      Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;

Query Match
Best Local Similarity 100.0%; Score 1377; DB 5; Length 1377;
Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0;
Indels 0; Gaps 0

```

Qy	1	ATGGTCAGCTACTGGGACACCGGGGTCTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTTC	60
Db	1	ATGGTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTCTTC	60
Qy	61	ACAGGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC	120
Db	61	ACAGGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC	120
Qy	121	CCGGAATTTATACATGACTGATGAAGGAGGAGCTCGTCAATTCCTGCGGGTTAGCTCA	180
Db	121	CCGGAATTTATACATGACTGAAGGAGGAGCTCGTCAATTCCTGCGGGTTAGCTCA	180
Qy	181	CTTAACATCACCTGTTTACTTTAAAAAGTTTCCACTTGACACTTTTGATTCCTCGATGAAAA	240
Db	181	CTTAACATCACCTGTTTACTTTAAAAAGTTTCCACTTGACACTTTTGATTCCTCGATGAAAA	240
Qy	241	CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGACTCAAGAAATA	300
Db	241	CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGACTCAAGAAATA	300
Qy	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTGTATTAAGCAAACTATCTCA	360
Db	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTGTATTAAGCAAACTATCTCA	360
Qy	361	CATCGACAAACCAATPACAAATCATAGATGTGGTCTCTGAGTCCGTCTCATTGGAAATGAACTA	420
Db	361	CATCGACAAACCAATPACAAATCATAGATGTGGTCTCTGAGTCCGTCTCATTGGAAATGAACTA	420
Qy	421	TCGTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGAA	480
Db	421	TCGTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACTAAATGTGGGAA	480
Qy	481	GACTTCAACTGGGAATACCCTTCTTGAAGCATCAGCATAAAGAACTTTGTAACCGAGAC	540
Db	481	GACTTCAACTGGGAATACCCTTCTTGAAGCATCAGCATAAAGAACTTTGTAACCGAGAC	540
Qy	541	CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGT	600
Db	541	CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGT	600
Qy	601	GTAACCCGGAGTGACCAAGGATTCGACCTGTGCGATCCAGTGGGCTGATGCCAAG	660
Db	601	GTAACCCGGAGTGACCAAGGATTCGACCTGTGCGATCCAGTGGGCTGATGCCAAG	660
Qy	661	AAGAAACAGCACATTTGTCAAGGTCATGAAAGGACAAAACTCACAATGCCCAACCGTGC	720
Db	661	AAGAAACAGCACATTTGTCAAGGTCATGAAAGGACAAAACTCACAATGCCCAACCGTGC	720
Qy	721	CCAACACCTGAACCTCTGGGGGACGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGAC	780
Db	721	CCAACACCTGAACCTCTGGGGGACGTCAGTCTTCTCTTCCCCCAAAACCCCAAGGAC	780
Qy	781	ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGTGTGAGCTGAGCCACGAA	840
Db	781	ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGTGTGAGCTGAGCCACGAA	840
Qy	841	GACCTGAGGTCAAGTTCAATGTTACGTGGAAGGCGTGTGAGTGTCAATATGCCAAGACA	900
Db	841	GACCTGAGGTCAAGTTCAATGTTACGTGGAAGGCGTGTGAGTGTCAATATGCCAAGACA	900



XX Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.

XX Example 20; Fig 24A-C; 179pp; English.

XX The present invention describes a method for treating psoriasis and  
CC enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antiinflammatory, vulnerary, antiaesthetic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related  
CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes VEGFR1R2-  
CC or FCDELTA1(a) which is used in an example from the present invention  
XX

SQ Sequence 1377 BP; 386 A; 374 C; 339 G; 278 T; 0 U; 0 Other;

Query Match 100.0%; Score 1377; DB 6; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTCGCGCTGCTCAGCTGCTGCTTC 60  
DB 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTCGCGCTGCTCAGCTGCTGCTTC 60  
QY 61 ACAGGATCTAGTTCGGAGTATACCGGTAGACCTTTCTGATAGATGTACAGTGAATC 120  
DB 61 ACAGGATCTAGTTCGGAGTATACCGGTAGACCTTTCTGATAGATGTACAGTGAATC 120  
QY 121 CCGAAATATATACATGACTGAAGGAGGGAGCTCGTCAATTCCTCGCGGTACGTCA 180  
DB 121 CCGAAATATATACATGACTGAAGGAGGGAGCTCGTCAATTCCTCGCGGTACGTCA 180  
QY 181 CTTAATCATCATCTTTACTTTAAATAAGTTTCCACTTGAACATTCCTGATGGAATA 240  
DB 181 CTTAATCATCATCTTTACTTTAAATAAGTTTCCACTTGAACATTCCTGATGGAATA 240  
QY 241 CGCATAATCTGGACAGTGAAGGGCTTCATCATATCAATGCAACGTACAAGAAATA 300  
DB 241 CGCATAATCTGGACAGTGAAGGGCTTCATCATATCAATGCAACGTACAAGAAATA 300  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGCTCAATGGGCATTTGTATAGACAAACTATCTACA 360  
DB 301 GGGCTTCTGACCTGTGAAGCAACAGCTCAATGGGCATTTGTATAGACAAACTATCTACA 360  
QY 361 CATGACAAAACCAATCAATCATAGATGTGTTCTGAGTCCGTCTCATGGAATTTGAATA 420  
DB 361 CATGACAAAACCAATCAATCATAGATGTGTTCTGAGTCCGTCTCATGGAATTTGAATA 420  
QY 421 TCTGTTGAGAAAAGCTTTGTCTTAAATTTGTACAGCAAGAACTTAAATTTGGGGATT 480  
DB 421 TCTGTTGAGAAAAGCTTTGTCTTAAATTTGTACAGCAAGAACTTAAATTTGGGGATT 480  
QY 481 GACTTCAACTGGGAATACCTTTCTCGAAGCATCAGCATAGAACTTGTAAACCGGAC 540  
DB 481 GACTTCAACTGGGAATACCTTTCTCGAAGCATCAGCATAGAACTTGTAAACCGGAC 540  
QY 541 CTTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAATATAGATGGT 600  
DB 541 CTTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAATATAGATGGT 600  
QY 601 GTAACCCGGAGTGACCAAGGATTTGTACACCTGTGACGATCATCAGTGGGCTGATGACCAAG 660  
DB 601 GTAACCCGGAGTGACCAAGGATTTGTACACCTGTGACGATCATCAGTGGGCTGATGACCAAG 660

QY 661 AAGAACAGCACAATTTGTTCAGGGTCCATGAAAGGACAAAACCTACACATGCCACCGTGC 720  
DB 661 AAGAACAGCACAATTTGTTCAGGGTCCATGAAAGGACAAAACCTACACATGCCACCGTGC 720  
QY 721 CCAGCACCTGAATCTCTGGGGGACCGGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
DB 721 CCAGCACCTGAATCTCTGGGGGACCGGTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780  
QY 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACTGCGTGGTGGTGGAGCTGAGCCACGAA 840  
DB 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACTGCGTGGTGGTGGAGCTGAGCCACGAA 840  
QY 841 GACCTCTGAGGTCAAGTTCAACTGCTGACCGCGCTGGAGGTGCATAATGCCAAGACA 900  
DB 841 GACCTCTGAGGTCAAGTTCAACTGCTGACCGCGCTGGAGGTGCATAATGCCAAGACA 900  
QY 901 AAGCGCGGGAGGAGAGTACAAACAGCAGCTGACCGTGGTGGTGGTGGTGGTGGTGGTGGT 960  
DB 901 AAGCGCGGGAGGAGAGTACAAACAGCAGCTGACCGTGGTGGTGGTGGTGGTGGTGGTGGT 960  
QY 961 CACCAGGACTGGCTGAAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCCA 1020  
DB 961 CACCAGGACTGGCTGAAATGGCAAGGAGTACAAAGTGCAGAGTCTCCAAACAAAGCCCTCCCA 1020  
QY 1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTAC 1080  
DB 1021 GCCCCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACACACAGGTGTAC 1080  
QY 1081 ACCCTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTGAGCTGACCTGCTGTC 1140  
DB 1081 ACCCTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTGAGCTGACCTGCTGTC 1140  
QY 1141 AAGGCTTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGGACCGCGAGAAC 1200  
DB 1141 AAGGCTTCTATCCAGGACATCCCGTGGAGTGGGAGAGCAATGGGACCGCGAGAAC 1200  
QY 1201 AACTACAAGACACCGCTCCCGTCTGGACTCCGACCGCTCTCTCTCTCTCTCTCTCTCTCT 1260  
DB 1201 AACTACAAGACACCGCTCCCGTCTGGACTCCGACCGCTCTCTCTCTCTCTCTCTCTCTCT 1260  
QY 1261 CTCAACCTGGACAAAGAGAGAGTGGCAGCAGGGGAAACGTTCTCATGCTCCGTTGATGAT 1320  
DB 1261 CTCAACCTGGACAAAGAGAGAGTGGCAGCAGGGGAAACGTTCTCATGCTCCGTTGATGAT 1320  
QY 1321 GAGGCTCTGCACACCACTACACCGCAGAGAGCTCTCCCTGCTCTCCGGGTAAATGA 1377  
DB 1321 GAGGCTCTGCACACCACTACACCGCAGAGAGCTCTCCCTGCTCTCCGGGTAAATGA 1377

RESULT 3

AAA91074

ID AAA91074 standard; DNA; 1453 BP.

XX

AC AAA91074;

XX

DT 05-APR-2001 (first entry)

XX

DE Flt1 receptor fusion protein Flt1D2.Flt1D3.FcDeltaC1(a) coding sequence.

XX

KW Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;

XX

KW plasma leakage; vascular permeability; IgG Fc region; ss.

XX

OS Unidentified.

XX

FN WO200075319-A1.

XX

PD 14-DEC-2000.

XX

PF 23-MAY-2000; 2000WO-US014142.

XX

PR 08-JUN-1999; 99US-0138133P.

XX



Key Location/Qualifiers  
CDS 69..1445  
/\*tag= a  
/product= "FltID2.FlkID3.FcDELTA1(a) "

WO200260489-A1.

08-AUG-2002.

28-JAN-2002; 2002WO-US002466.

31-JAN-2001; 2001US-00773877.

(REGE-) REGENERON PHARM INC.

Xia Y, Rudge JS, Yancopoulos GD;

WPI; 2002-608488/65.

P-PSDB; ABP52447.

Treating psoriasis and enhancing wound healing in humans comprises the administration of a vascular endothelial cell growth factor (VEGF) antagonist.

Example 17; Fig 21A-C; 179pp; English.

The present invention describes a method for treating psoriasis and enhancing wound healing in a mammal or a human. The method comprises administering a vascular endothelial cell growth factor (VEGF) antagonist to the mammal or human. A VEGF antagonist has antipsoriatic, antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic, nephrotropic and ophthalmological activities. The method can be used in treating psoriasis and enhancing wound healing in humans by administering VEGF antagonist. The method is also useful in treating clinical conditions characterised by vascular permeability, oedema or inflammation, such as brain oedema associated with injury, oedema associated with inflammatory disorders (e.g. rheumatoid arthritis), asthma, burns, kidney diseases, or eye disorders such as age-related macular degeneration and diabetic retinopathy. The method may also be used in making the polypeptide to decrease or inhibit plasma leakage and or vascular permeability. The present sequence encodes FltID2.FlkID3.FcDELTA1(a) which is used in an example from the present invention

Sequence 1453 BP; 398 A; 400 C; 366 G; 289 T; 0 U; 0 Other;

Query Match 96.5%; Score 1328.4; DB 6; Length 1453;

Best Local Similarity 98.6%; Pred. No. 3e-312;

Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;

Qy	1	ATGGTCACGCTACTGGGACACCGGGTCTCTGTGCGCGCTGCTCAGCTGCTGCTTC	60
Db	69	ATGGTCACGCTACTGGGACACCGGGTCTCTGTGCGCGCTGCTCAGCTGCTGCTTC	128
Qy	61	ACAGGATCTAGTTCCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAAATC	120
Db	129	ACAGGATCTAGTTCCGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAAATC	179
Qy	121	CCGGAATATATACATGCTGAAGGAAGGAGTCTGTCATTCCTGCGGGTTACGTC	180
Db	180	CCGGAATATATACATGCTGAAGGAAGGAGTCTGTCATTCCTGCGGGTTACGTC	239
Qy	181	CCTAACATCACTGTACTTTTAAAGTTTCCACTTGACCTTTGATCCCTGATGGAAA	240
Db	240	CCTAACATCACTGTACTTTTAAAGTTTCCACTTGACCTTTGATCCCTGATGGAAA	299
Qy	241	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACAAAGAAATA	300
Db	300	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACAAAGAAATA	359
Qy	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAACTATCTACA	360
Db	360	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAACTATCTACA	419

Qy	361	CATCGAACAACAATAACAATCATAGATGTGGTCTTGAGTCCGTCTCATGGAATTGAACCTA	420
Db	420	CATCGAACAACAATAACAATCATAGATGTGGTCTTGAGTCCGTCTCATGGAATTGAACCTA	479
Qy	421	TCTGTGGAGAAAAAGCTTGTCTTAAATTTGTAACAGCAAGAACTGAACCTAAATGTGGGATT	480
Db	480	TCTGTGGAGAAAAAGCTTGTCTTAAATTTGTAACAGCAAGAACTGAACCTAAATGTGGGATT	539
Qy	481	GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAAGAACTTTGTAACCGAGAC	540
Db	540	GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAAGAACTTTGTAACCGAGAC	599
Qy	541	CTAAAAAACCAGTCTGGAGTGAGATGAAGAAAATTTTGTAGCACCTTAACCTATAGATGGT	600
Db	600	CTAAAAAACCAGTCTGGAGTGAGATGAAGAAAATTTTGTAGCACCTTAACCTATAGATGGT	659
Qy	601	GTAACCCCGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG	660
Db	660	GTAACCCCGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG	719
Qy	661	AAGAACAAGCATTTGTTCAGGTTCCATGAAAAG-----GACAAAACCTCACACATGC	711
Db	720	AAGAACAAGCATTTGTTCAGGTTCCATGAAAAGGGCCCGGGCGACAAAACCTCACACATGC	779
Qy	712	CCACCGTCCCGAGCACCTGAACTCTCGGGGGACCGTCAAGTCTTCTTCCCTCCCAAAA	771
Db	780	CCACCGTCCCGAGCACCTGAACTCTCGGGGGACCGTCAAGTCTTCTTCCCTCCCAAAA	839
Qy	772	CCCAAGGACACCTCATGATCTCCCGGACCCCTCAGAGTCAATGCGTGGTGGTGGACGTG	831
Db	840	CCCAAGGACACCTCATGATCTCCCGGACCCCTCAGAGTCAATGCGTGGTGGTGGACGTG	899
Qy	832	AGCCACAAGACCTTAGGTTCACTGTTCACTGTTAGCTGAGCGCGGTGGAGTGCATAT	891
Db	900	AGCCACAAGACCTTAGGTTCACTGTTCACTGTTAGCTGAGCGCGGTGGAGTGCATAT	959
Qy	892	GCCAAGACAAAGCCCGGGAGGACGATACAAACAGCAGCTACCGTGGTGGTGGTGGTCTC	951
Db	960	GCCAAGACAAAGCCCGGGAGGACGATACAAACAGCAGCTACCGTGGTGGTGGTGGTCTC	1019
Qy	952	ACCGTCTTCGACCAAGGATCGCTGTAATGGCAAGAGGTACAAAGTCTCAACAAA	1011
Db	1020	ACCGTCTTCGACCAAGGATCGCTGTAATGGCAAGAGGTACAAAGTCTCAACAAA	1079
Qy	1012	GCCCTCCCGAGCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGAACCA	1071
Db	1080	GCCCTCCCGAGCCCATCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCGGAGAACCA	1139
Qy	1072	CAGGTGTACACCTTCCCGGATGAGTGAACCAAGAACCAAGGTGAGGAGCAATGGGCGAG	1131
Db	1140	CAGGTGTACACCTTCCCGGATGAGTGAACCAAGAACCAAGGTGAGGAGCAATGGGCGAG	1199
Qy	1132	TGCTGTGTAAGAGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGAG	1191
Db	1200	TGCTGTGTAAGAGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGAG	1259
Qy	1192	CCGGAAGAACCTAACAGACACCGCTCCCGTGGTGGATCCCGAGCGGCTCTTCTTCTC	1251
Db	1260	CCGGAAGAACCTAACAGACACCGCTCCCGTGGTGGATCCCGAGCGGCTCTTCTTCTC	1319
Qy	1252	TACAGCAAGCTCACCGTGGACAAAGAGCAGTGGCGAGCAGGGGACGCTTCTCATGCTCC	1311
Db	1320	TATAGCAAGCTCACCGTGGACAAAGAGCAGTGGCGAGCAGGGGACGCTTCTCATGCTCC	1379
Qy	1312	GTGATGATGAGGCTCTGCAACCAACCTACACGCAAGAGCGCTCTCCCTGTCTCCGGGT	1371
Db	1380	GTGATGATGAGGCTCTGCAACCAACCTACACGCAAGAGCGCTCTCCCTGTCTCCGGGT	1439
Qy	1372	AAATGA 1377	
Db	1440	AAATGA 1445	





QY 1072 CAGGTGTACACCTGCGCCCTCCCGGATGAGCTGACCAAGAACAGGTGAGCTGACC 1131  
DB |  
QY 1131 CAGGTGTACACCTGCGCCCTCCCGGATGAGCTGACCAAGAACAGGTGAGCTGACC 1190  
DB |  
QY 1132 TGCTGTGTCAAAGGCTTCTATCCCAAGCAGCATCGCGTGGAGTGGAGCAATGGGCAG 1191  
DB |  
QY 1191 TGCTGTGTCAAAGGCTTCTATCCCAAGCAGCATCGCGTGGAGTGGAGCAATGGGCAG 1250  
DB |  
QY 1192 CCGGAGAACACTACAGACCAAGCCTCCCGTGTGGACTCGAGCGGCTCTTCTTCTC 1251  
DB |  
QY 1251 CCGGAGAACACTACAGACCAAGCCTCCCGTGTGGACTCGAGCGGCTCTTCTTCTC 1310  
DB |  
QY 1252 TACAGCAAGCTCACCGTGCACAGAGCAGTGGCAGAGGGGAAAGCTTCTCTCATGTCTCC 1311  
DB |  
QY 1311 TATAGCAGCTCACCGTGCACAGAGCAGTGGCAGAGGGGAAAGCTTCTCTCATGTCTCC 1370  
DB |  
QY 1312 GTGATGATAGGCTTGTSCAACACCATACACGAGAGAGCCCTCTCCCTGTCTCCGGGT 1371  
DB |  
QY 1371 GTGATGATAGGCTTGTSCAACACCATACACGAGAGAGCCCTCTCCCTGTCTCCGGGT 1430  
DB |  
QY 1372 AAATGA 1377  
DB |  
QY 1431 AAATGA 1436  
DB |

## RESULT 7

AAA91071  
ID AAA91071 standard; DNA; 1359 BP.

AC AAA91071;

DT 05-APR-2001 (first entry)

XX Ftl1 receptor fusion protein Mut2:Ftl1(2-3deltaB)-Fc coding sequence.

DE Ftl1 receptor; fusion protein; chimeric protein; IgG Fc region; ss.

KW plasma leakage; vascular permeability; IgG Fc region; ss.

XX Unidentified.

XX Key

FH Location/Qualifiers

FT 1. 1359

FT /\*tag= a

FT /product= "Ftl1(2-3deltaB)-Fc"

XX WO200075319-A1.

XX 14-DEC-2000.

XX 23-MAY-2000; 2000WO-US014142.

XX 08-JUN-1999; 99US-0138133P.

XX (REGE-) REGENERON PHARM INC.

XX Papadopoulos NJ, Davis S, Yancopoulos GD;

XX WPI; 2001-071076/08.

DR P-PSDB; AAY97591.

XX Nucleic acid molecule encoding mammalian phospholipid transfer protein, and its fragments, useful for diagnosis, evaluation, and treatment of diseases associated with the gene expression and for producing model systems.

XX Claim 9; Fig 14; 159pp; English.

XX This sequence encodes a fusion protein of the invention between the Ftl1 receptor and the Fc region of IgG. The specification relates to modified chimeric polypeptides with improved pharmacokinetics. The modified chimeric polypeptides are preferably Ftl1 receptor polypeptides that have been modified to improve their pharmacokinetic profile. The polypeptides can be used to decrease or inhibit plasma leakage and/or vascular

CC permeability in a mammal

XX Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;

Query Match 75.5%; Score 1039; DB 5; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 5.3e-242;  
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

QY 1 ATGCTCAGCTACTGGGACACGGGGTCTCTGCTGCGCGCTGCTCAGCTGCTGCTCTC 60

DB 1 ATGCTCAGCTACTGGGACACGGGGTCTCTGCTGCGCGCTGCTCAGCTGCTGCTCTC 60

QY 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120

DB 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 111

QY 121 CCGAATATTATACATGACTGAAGGAAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 180

DB 121 CCGAATATTATACATGACTGAAGGAAGGAGCTCGTCAATTCCTGCGGGTTACGTCA 171

QY 181 CTTAATCATCTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 240

DB 172 CTTAATCATCTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 231

QY 241 CGCATATCTGGGACAGTGAAGGGCTTCCATCATATCAATCAAGTCAAGGAATA 300

DB 232 CGCATATCTGGGACAGTGAAGGGCTTCCATCATATCAATCAAGTCAAGGAATA 291

QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACA 360

DB 292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTCACA 351

QY 361 CATCGCAAAACCAATACATCATAGATGTGGTCTGAGTCCGCTCATGGAATGAACTA 420

DB 352 CATCGCAAAACCAATACATCATAGATGTGGTCTGAGTCCGCTCATGGAATGAACTA 411

QY 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGACAGCAAGAACTGAACATAATGTGGGATT 480

DB 412 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGACAGCAAGAACTGAACATAATGTGGGATT 471

QY 481 GACTTCAACTGGGAATACCTCTTTCGAAGCATCAGCATTAAGAACTTTGTAACCGGAC 540

DB 472 CAAATGACCTGGAGTTACCTCTGATGAAATTTGACAAAGCAATTTCCCATGCAACATATTC 531

QY 541 CTAAAAACCCAGTCTGGGAGTGAATGAAGAAATTTTGGAGCACTTAACTATAGATGTT 600

DB 532 TACAGTGTCTTACTATTTGACAAATTTGACAAAGCAAGAACTTTTACTTTGCTGTT 591

QY 601 GTAAACCGGAGTGACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660

DB 592 GTAA---GGAGTGAGCCATCTTCAATCTGTTAAACCTC-----AGTGCAATATAT 642

QY 661 AAGAACAGCAATTTGTGAGGTCCTTCAATGAAAGGACAAACTCACAATGCCACCGTGC 720

DB 643 GATAAAGCAGCGCGCGGAGCCCAATCTTGTGACAAAACTCACAATGCCACCGTGC 702

QY 721 CCAGCACCTGAATCTCTGGGGGACCGTCACTTCTTCTTCCCTCCCAAAACCCAGGAC 780

DB 703 CCAGCACCTGAATCTCTGGGGGACCGTCACTTCTTCTTCCCTCCCAAAACCCAGGAC 762

QY 781 ACCCTCATGATCTCCGGACCCCTGAGGTCAATGCGTGTGGTGGAGTGGAGCCAGAA 840

DB 763 ACCCTCATGATCTCCGGACCCCTGAGGTCAATGCGTGTGGTGGAGTGGAGCCAGAA 822

QY 841 GACCTGAGGTCAAGTTCAAAGTGTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 900

DB 823 GACCTGAGGTCAAGTTCAAAGTGTGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 882

QY 901 AAGCCGGGAGGAGGAGTGAACAGCAAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGT 960

DB 883 AAGCCGGGAGGAGGAGTGAACAGCAAGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGT 942

QY 961 CACCAGGACTGGGTGAATGGCAAGGAGTACAAGTGAAGTCTCCAAAGAGGCTCCCA 1020



Db 943 CACCGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGCTCCAAACAAAGCCCTCCCA 1002  
 Qy 1021 GCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCACAGGTGTAC 1080  
 Db 1003 GCGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCACAGGTGTAC 1062  
 Qy 1081 ACCCTGCCCCATCCCGGATGAGTGAACCAAGAACCCAGGTGAGCTTCCCTGCTGTC 1140  
 Db 1063 ACCCTGCCCCATCCCGGATGAGTGAACCAAGAACCCAGGTGAGCTTCCCTGCTGTC 1122  
 Qy 1141 AAAGGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGGAGCCGAGAAC 1200  
 Db 1123 AAAGGCTTCTATCCAGGACATCCCGTGGAGTGGAGAGCAATGGGAGCCGAGAAC 1182  
 Qy 1201 AACTACAAGACCAACCCCTCCCGTGGTGGACTCCGAGCGCTCTTCTTCTTACAGCAAG 1260  
 Db 1193 AACTACAAGACCAACCCCTCCCGTGGTGGACTCCGAGCGCTCTTCTTCTTACAGCAAG 1242  
 Qy 1261 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTTCTTCATGCTCCGTGATGCAT 1320  
 Db 1243 CTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTTCTTCATGCTCCGTGATGCAT 1302  
 Qy 1321 GAGGCTCTGCACAACCACTACACGAGAGAGCCTTCCCTGTCTCCGGGTAAATGA 1377  
 Db 1303 GAGGCTCTGCACAACCACTACACGAGAGAGCCTTCCCTGTCTCCGGGTAAATGA 1359

## RESULT 8

ABQ74605

ID ABQ74605 standard; cDNA; 1359 BP.

XX

XX

AC ABQ74605;

XX

DT 23-OCT-2002 (first entry)

XX

DE Mutation 2 Flt1(2-3 delta B)-Fc nucleotide sequence.

XX

XX Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;

KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;

KW vulnery; antiaesthetic; antirheumatic; antiarthritic; nephrotropic;

KW ophthalmological; vascular permeability; oedema; inflammation; asthma;

KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;

KW kidney disease; eye disorder; age-related macular degeneration;

KW diabetic retinopathy; gene; ss.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key

CDS Location/Qualifiers

FT 1..1359

FT /\*tag= a

FT /product= "Mut2:Flt1(2-3 delta B)-Fc protein"

FT

XX WO200260489-A1.

XX

XX 08-AUG-2002.

XX

XX 28-JAN-2002; 2002WO-US002466.

XX

XX 31-JAN-2001; 2001US-00773877.

XX

XX (REGE-) REGENERON PHARM INC.

XX

XX Xia Y, Rudge JS, Yancopoulos GD;

XX

XX WPI; 2002-608488/65.

XX

XX P-PSDB; ABP52444.

XX

XX Treating psoriasis and enhancing wound healing in humans comprises the

PT administration of a vascular endothelial cell growth factor (VEGF)

PT antagonist.

XX

## Example 12; Fig 14A-C; 179pp; English.

PS The present invention describes a method for treating psoriasis and  
 XX enhancing wound healing in a mammal or a human. The method comprises  
 CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
 CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
 CC antiinflammatory, vulnery, antiaesthetic, antirheumatic, antiarthritic,  
 CC nephrotropic and ophthalmological activities. The method can be used in  
 CC treating psoriasis and enhancing wound healing in humans by administering  
 CC VEGF antagonist. The method is also useful in treating clinical  
 CC conditions characterised by vascular permeability, oedema or  
 CC inflammation, such as brain oedema associated with injury, oedema  
 CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
 CC asthma, burns, kidney diseases, or eye disorders such as age-related  
 CC macular degeneration and diabetic retinopathy. The method may also be  
 CC used in making the polypeptide to decrease or inhibit plasma leakage and  
 CC or vascular permeability. The present sequence encodes Mut2:Flt1(2-3  
 CC delta B)-Fc which is used in an example from the present invention  
 XX

SQ Sequence 1359 BP; 381 A; 388 C; 314 G; 276 T; 0 U; 0 Other;

Query Match 75.5%; Score 1039; DB 6; Length 1359;

Best Local Similarity 86.3%; Pred. No. 5.3e-242;

Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

Qy 1 ATGGTCTAGTCTGGGACACCGGGGCTCTGCTGTGGCGGCTGCTCAGCTGTCTGCTTCTC 60

Db 1 ATGGTCTAGTCTGGGACACCGGGGCTCTGCTGTGGCGGCTGCTCAGCTGTCTGCTTCTC 60

Qy 61 ACAGGATCTAGTCTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120

Db 61 ACAGGATCTAGTCTCCGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 111

Qy 121 CCCGAAATTTACACATGACTGAAGGAAGGAGCTGCTCATTTCCCTGCCGGTTACGTCA 180

Db 112 CCCGAAATTTACACATGACTGAAGGAAGGAGCTGCTCATTTCCCTGCCGGTTACGTCA 171

Qy 181 CCTAACATCACTGTCTTTTAAAGGTTTCCACTTCACACTTTTGATCCCTGATGGAAA 240

Db 172 CCTAACATCACTGTCTTTTAAAGGTTTCCACTTCACACTTTTGATCCCTGATGGAAA 231

Qy 241 CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAAGCTACAAAGAAATA 300

Db 232 CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAAGCTACAAAGAAATA 291

Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 360

Db 292 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 351

Qy 361 CATCGACAAACCAATACAATCATAGATGTGTTCTGAGTCGCTCATGGAAATTTGAAC 420

Db 352 CATCGACAAACCAATACAATCATAGATGTGTTCTGAGTCGCTCATGGAAATTTGAAC 411

Qy 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGACGAAAGAACTGAACTAAATGTGGGATT 480

Db 412 CTTAGAGGCCATCTCTTGTCTCAATTTGTACTGCTACCACTCCCTTTGAACACGAGATT 471

Qy 481 GACTTCAACTGGGAATACCTCTTTCGAAGCATCAGCATTAAGAACTTTGTAACCCGAGAC 540

Db 472 CAAATGACCTGGAGTTTACCTCTGATGAAATTTGACCAAGCAATTTCCCATGCCAACATATTC 531

Qy 541 CTAAGAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGACCTTTAACTATAGATGGT 600

Db 532 TACAGTGTCTTACTATTGACAAATTCAGAAACCAAGCAAGAGCACTTTATCTTGTGCT 591

Qy 601 GTAAACCGGAGTGACCAAGGATTGTACACCTGTGAGCATCCAGTGGGGCTGATGACCAAG 660

Db 592 GTAA---GGAGTGGACCATCATTTCAATCTGTTAAACACCTC-----AGTGCATATAT 642

Qy 661 AAGAACAGCATTGTCAGGGTCCATGAAAGCAAAACTCACACATGCCACCGTGC 720

Db 643 GATAAAGCAGCGCGCGGAGCCCAATCTTGTGACAAAACTCACACATGCCACCGTGC 702



Db 646 TCTGTTAAACATCTGATGATATATATGATAAAGCAGGCGCCCGGCGAGCCCAAACTTTGT 705  
Qy 694 GACAAAACCTCACACATGCCACCGTCCAGCAGCACCTGAACTCCTCTGGGGGACCGTCAGTC 753  
Db 706 GACAAAACCTCACACATGCCACCGTCCAGCAGCACCTGAACTCCTGGGGGACCGTCAGTC 765  
Qy 754 TTCCTCTTCCCGCCCAAAACCCCAAGGACACCTCTCATGATCTCCCGGACCCCTGAGGTACCA 813  
Db 766 TTCTCTTTCCCGCCCAAAACCCCAAGGACACCTCTCATGATCTCCCGGACCCCTGAGGTACCA 825  
Qy 814 TCGTGTGGTGGAGCTGAGGCCACCAAGACCCCTGAGGTCAAGTTCAACTGTTGACGTGAC 873  
Db 826 TCGTGTGGTGGAGCTGAGGCCACCAAGACCCCTGAGGTCAAGTTCAACTGTTGACGTGAC 885  
Qy 874 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTCAACACAGCACGTCAC 933  
Db 886 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTCAACACAGCACGTCAC 945  
Qy 934 COTGTGGTCAGCGTCTCTCACCGTCTCTGCACAGGACTGGCTGTAATGGCAAGGAGTACAA 993  
Db 946 CGTGTGGTCAGCGTCTCTCACCGTCTCTGCACAGGACTGGCTGTAATGGCAAGGAGTACAA 1005  
Qy 994 TCCAAAGGTCTCCAAACAAAGCCCTCCAGGCCCTCATCGAGAAACCATCTCCAAAGCCAAA 1053  
Db 1006 TCCAAAGGTCTCCAAACAAAGCCCTCCAGGCCCTCATCGAGAAACCATCTCCAAAGCCAAA 1065  
Qy 1054 GGGCAGCCCGCAGAACCCAGCTGTACACCTGCCCGCCCATCCCGGATGAGTACCAAG 1113  
Db 1066 GGGCAGCCCGCAGAACCCAGCTGTACACCTGCCCGCCCATCCCGGATGAGTACCAAG 1125  
Qy 1114 AACCAAGGTCTCAGCTGCTGCTGCTCAAGAGCTTCTATCCAGCGCATCGCGCTGAG 1173  
Db 1126 AACCAAGGTCTCAGCTGCTGCTGCTCAAGAGCTTCTATCCAGCGCATCGCGCTGAG 1185  
Qy 1174 TGGGAGACCAATGGCAGCCGAGAACCACTACAGACACGCTTCCCGTGTGACATCC 1233  
Db 1186 TGGGAGACCAATGGCAGCCGAGAACCACTACAGACACGCTTCCCGTGTGACATCC 1245  
Qy 1234 GAGGCTCTTCTTCTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGCACGAGGG 1293  
Db 1246 GAGGCTCTTCTTCTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGCACGAGGG 1305  
Qy 1294 AACGCTTCTCTCATGCTCCGCTGATGATGATGAGGCTCTGCAACCACTACACGAGAGC 1353  
Db 1306 AACGCTTCTCTCATGCTCCGCTGATGATGATGAGGCTCTGCAACCACTACACGAGAGC 1365  
Qy 1354 CTCTCCCTGTCTCCGGGTAATGA 1377  
Db 1366 CTCTCCCTGTCTCCGGGTAATGA 1389

RESULT 10

ABQ74606  
ID ABQ74606 standard; cDNA; 1389 BP.

AC ABQ74606;

DT 23-OCT-2002 (first entry)

DE Mutation 3 Flt1(2-3)-Fc nucleotide sequence.

KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnary; antiaesthetic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy; gene; ss.

OS Homo sapiens.

OS Synthetic.

XX

Key Location/Qualifiers  
CDS 1..1389  
/\*tag= a  
/product= "Mut3:Flt1(2-3)-Fc protein"

PN WO200260489-A1.

PD 08-AUG-2002.

PF 28-JAN-2002; 2002WO-US002466.

PR 31-JAN-2001; 2001US-00773877.

PA (REG- ) REGENERON PHARM INC.

PI Xia Y, Rudge JS, Yancopoulos GD;

DR WPI; 2002-608488/65.

XX Treating psoriasis and enhancing wound healing in humans comprises the  
PT administration of a vascular endothelial cell growth factor (VEGF)  
PT antagonist.

XX Example 13; Fig 15A-C; 179pp; English.

PS The present invention describes a method for treating psoriasis and  
XX enhancing wound healing in a mammal or a human. The method comprises  
CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
CC antiinflammatory, vulnary, antiaesthetic, antirheumatic, antiarthritic,  
CC nephrotropic and ophthalmological activities. The method can be used in  
CC treating psoriasis and enhancing wound healing in humans by administering  
CC VEGF antagonist. The method is also useful in treating clinical  
CC conditions characterised by vascular permeability, oedema or  
CC inflammation, such as brain oedema associated with injury, oedema  
CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
CC asthma, burns, kidney diseases, or eye disorders such as age-related  
CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes Mut3:Flt1(2-3)-Fc  
CC which is used in an example from the present invention

SQ Sequence 1389 BP; 394 A; 393 C; 322 G; 280 T; 0 U; 0 Other;

Query Match 75.0%; Score 1032.4; DB 6; Length 1389;

Best Local Similarity 85.5%; Pred. No. 2.2e-240;

Matches 1201; Conservative 0; Mismatches 161; Indels 42; Gaps 3;

Qy 1 ATGCTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTC 60  
Db 1 ATGCTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGCTGCTCAGCTGTCTGCTTC 60

Qy 61 ACAGGATCTAGTTCGGAAAGTGATACCGGTAGACCTTTGTPAGAGATGACAGTGAATC 120

Db 61 ACAGGATCTAGTTCGGAAAGTGATACCGGTAGACCTTTGTPAGAGATGACAGTGAATC 111

Qy 121 CCGGAAATATACATGATCTGAGGAGGGAGCTCGTTCATCCCTCCGGGTACGTCAC 180

Db 112 CCGGAAATATACATGATCTGAGGAGGGAGCTCGTTCATCCCTCCGGGTACGTCAC 171

Qy 181 CCTAACATCACTGTACTTTTAAAAAGTTTCCACTGCACCTTTGATCCCTGATGGAAAA 240

Db 172 CCTAACATCACTGTACTTTTAAAAAGTTTCCACTGCACCTTTGATCCCTGATGGAAAA 231

Qy 241 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATCAAGTCAAGAGTCAAGAGAAATA 300

Db 232 CGCATATCTGGGACAGTGAAGGGCTTCATCATATCAATCAAGTCAAGAGTCAAGAGAAATA 291

Qy 301 GGGCTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 360

Db 292 GGGCTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTATCTACA 351

Qy 361 CATCGACAAACCAATACATAGATGTGGTCTGAGTCCGTCTCATGGAAATGAACTA 420

Db 352 CATCGACAAACCAATACATCATAGATGTCMAATTAAGCACCACGCCAGTCAAAATTA 411  
Qy 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACATAATGTGGGATT 480  
Db 412 CTTAGAGGCCATACCTTGTCTCAATTTGTACTGCTACCACTCCCTTTGAACACGAGAGTT 471  
Qy 481 GACTTCAACTGGGAATACCTTCTTGNAGCATCAGCATAGAAGAACTTTGAACCGGAGAC 540  
Db 472 CAAATGACCTGGAGTTACCTCT-----GATGAAAAAATAAGAGAGCTTCGGTAAGCGGA 525  
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACCTATAGATGTT 600  
Db 526 CGAATTGACCAAGCAATCCATGCCAAATATCTACAGTGTCTTACTATTTGACAAA 585  
Qy 601 GTAAACCCGGAGTGACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Db 586 ATGCAGAACAAAGACAAAGGACTTTATACCTTGTGTTAGGAGTGGACCATCATTTCAA 645  
Qy 661 AAGAACAGCATTGTCTCAGGCTCATGAATA-----G 693  
Db 646 TCTGTTAAACCTCAGTGCATATATATATAAGCAGGCCCGCGGAGCCCAATCTTGT 705  
Qy 694 GACAAACTCACATGCCACCTGCCAGCACCTGAACCTCTCTGGGGGACCTCAGTC 753  
Db 706 GACAAACTCACATGCCACCTGCCAGCACCTGAACCTCTCTGGGGGACCTCAGTC 765  
Qy 754 TTCTCTTCCCCCAAAACCAAGGACACCTCTATGATCTCCCGGACCCCTGAGGTCAACA 813  
Db 766 TTCTCTTCCCCCAAAACCAAGGACACCTCTATGATCTCCCGGACCCCTGAGGTCAACA 825  
Qy 814 TCGTGTGTGTGGAGTGGAGCCAGAGACCTCTGAGGTCAAGTTCAACTGTGAGTGGAC 873  
Db 826 TGCCTGTGTGTGGAGTGGAGCCAGAGACCTCTGAGGTCAAGTTCAACTGTGAGTGGAC 885  
Qy 874 GCGTGTGAGGTGCATTAATGCCAAGCAAGCCGCGGAGGAGCAGTCAACAGCACCTGAC 933  
Db 886 GCGTGTGAGGTGCATTAATGCCAAGCAAGCCGCGGAGGAGCAGTCAACAGCACCTGAC 945  
Qy 934 CGTGTGTGTGAGTGTCTCACCGTCTCTGCACAGGAGTGGCTGAATGGCAAGGAGTACAAG 993  
Db 946 CGTGTGTGTGAGTGTCTCACCGTCTCTGCACAGGAGTGGCTGAATGGCAAGGAGTACAAG 1005  
Qy 994 TGCAGGTCTTCAACAAGGCCCTCCAGCCGCCATCGAGAAACGATCTCCAAAGCCAAA 1053  
Db 1006 TGCAGGTCTTCAACAAGGCCCTCCAGCCGCCATCGAGAAACGATCTCCAAAGCCAAA 1065  
Qy 1054 GGGCAGCCCGCAGAACACAGGTGTACACCTCTGCCCCCATCCCGGATGAGCTGACCAAG 1113  
Db 1066 GGGCAGCCCGCAGAACACAGGTGTACACCTCTGCCCCCATCCCGGATGAGCTGACCAAG 1125  
Qy 1114 AACAGGTTCAGCTGACCTGCTGTCTGCTCAAGGCTTCTATCCAGCGACATCCCGGTGGAG 1173  
Db 1126 AACAGGTTCAGCTGACCTGCTGTCTGCTCAAGGCTTCTATCCAGCGACATCCCGGTGGAG 1185  
Qy 1174 TGGAGAGCAATGGCAGCCCGAGAAACAACTACAGACACGCTCCCGTCTGACTGCC 1233  
Db 1186 TGGAGAGCAATGGCAGCCCGAGAAACAACTACAGACACGCTCCCGTCTGACTGCC 1245  
Qy 1234 GACGCTCTTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGG 1293  
Db 1246 GACGCTCTTCTTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGG 1305  
Qy 1294 AACGCTCTTCTATGCTCCGCTGATGATGAGGCTCTTGCAACCACTACACGAGAAGAGC 1353  
Db 1306 AACGCTCTTCTATGCTCCGCTGATGATGAGGCTCTTGCAACCACTACACGAGAAGAGC 1365  
Qy 1354 CTCTCCCTGTCTCCGGTAAATGA 1377  
Db 1366 CTCTCCCTGTCTCCGGTAAATGA 1389

RESULT 11

AAA91070  
ID AAA91070 standard; DNA; 1674 BP.  
XX  
XX AAA91070;  
XX AC  
XX XX  
DT 05-APR-2001 (first entry)  
XX  
XX Flt1 receptor fusion protein Mutl:Flt1(1-3deltaB)-Fc coding sequence.  
XX  
XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
KW plasma leakage; vascular permeability; IgG Fc region; ss.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
FT CDS 1..1674  
FT FT /\*tag= a  
FT FT /product= "Flt1(1-3deltaB)-Fc"  
XX  
XX W0200075319-A1.  
XX  
XX 14-DEC-2000.  
XX  
XX 23-MAY-2000; 2000WO-US014142.  
XX  
XX 08-JUN-1999; 99US-0138133P.  
XX  
XX (REGE-) REGENERON PHARM INC.  
XX  
XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
XX WPI; 2001-071076/08.  
DR P-PSDB; AAY97590.  
XX  
XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems.  
XX  
XX Claim 9; Fig 13; 159pp; English.  
XX  
XX This sequence encodes a fusion protein of the invention between the Flt1  
CC receptor and the Fc region of IGG. The specification relates to modified  
CC chimeric polypeptides with improved pharmacokinetics. The modified  
CC chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
CC been modified to improve their pharmacokinetic profile. The polypeptides  
CC can be used to decrease or inhibit plasma leakage and/or vascular  
CC permeability in a mammal  
XX  
SQ Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;  
  
Query Match 71.7%; Score 987.4; DB 5; Length 1674;  
Best Local Similarity 86.1%; Pred. No. 1.9e-229;  
Matches 1119; Conservative 0; Mismatches 171; Indels 9; Gaps 2;  
  
Qy 79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTCAAAATCCCCGAAATATACACATG 138  
Db 385 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTCAAAATCCCCGAAATATACACATG 444  
Qy 139 ACTGAAGGAGGAGCTCGTCATTCCCTGCCGGGTACGTCACCTAACATCCTGTTACT 198  
Db 445 ACTGAAGGAGGAGCTCGTCATTCCCTGCCGGGTACGTCACCTAACATCCTGTTACT 504  
Qy 199 TTAAGAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAAACGCAATCTGGGACAGT 258  
Db 505 TTAAGAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAAACGCAATCTGGGACAGT 564  
Qy 259 AGAAGGGCTTCATCATATCAATGCAACGCTACAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db 565 AGAAGGGCTTCATCATATCAATGCAACGCTACAAAGAAATAGGCTTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCTTTGTATAAGACAAATCTCTCACATCGACAAACCAATACA 378

Db 625 GCAACAGTCAATGGGCAATTGTATAGACAAACTATCTCACACATCGACAAACCAATACA 684  
Qy 379 ATCATAGATGTGGTCTGAGTCCGCTCATGAAATTGAACTATCTGTTGGAGAAAGCTT 438  
Db 685 ATCATAGATGTCAATAAGACACACGCCCGCTCAAAATTACTTAGAGGCCATCTCTT 744  
Qy 439 GTCTTAATTTGACAGCAAGAACTGAACCTAAATGTGGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTCAATTTGACTGTACCACTCCCTTGAACACGAGAGTTTCAATGACCTGGAGTTAC 804  
Qy 499 CTTCTTGAAGCATCAGATGAAGAACTGTGTAACCGAGACTAAACCCAGCTGGG 558  
Db 805 CTTGATGAATTTGACCAAGCAATTTCCCATGCAACATATTACAGTGTCTTCTTACTT 864  
Qy 559 AGTGAGATGAAGAAATTTTGTAGACCTTTAACTATAGATGGTGTAAACCGGAGTGACCAA 618  
Db 865 GACAAATGCAGACAAAGACAAAGGACTTTATCTTGTGCTGTAA---GGAGTGACCA 921  
Qy 619 GGATTTGACCTGTGCAGCTCCAGTGGGCTGTATGACCAAGAAAGACGACATTTGTC 678  
Db 922 TCATTTCAATCTGTTAAACACCTC-----AGTGCATATATATGATAAAGCAGGCCCGGC 975  
Qy 679 AGGTGTCATGAAGAGCAAAACTCACATGCCACCGTCCAGCAGCTGAATCTCTG 738  
Db 976 GAGCCCAATCTTGTGACAAACTCACACATGCCACCGTCCAGCAGCTGAATCTCTG 1035  
Qy 739 GGGGACCGTCAAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCGG 798  
Db 1036 GGGGACCGTCAAGTCTTCTCTTCCCTCCCAAAACCAAGGACACCTCATGATCTCCGG 1095  
Qy 799 ACCCTGAGGTCACTGCTGTGTGTGGACGTGAGCCACGAAGACCTTGAGTCAAGTTC 858  
Db 1096 ACCCTGAGGTCACTGCTGTGTGTGGACGTGAGCCACGAAGACCTTGAGTCAAGTTC 1155  
Qy 859 AACTGTTAGTGGACGGCGTGGAGTGCATTAATGCAAGAAAGCCGGGAGAGCAG 918  
Db 1156 AACTGTTAGTGGACGGCGTGGAGTGCATTAATGCAAGAAAGCCGGGAGAGCAG 1215  
Qy 919 TACACAGCAGTACCGTGTGTGTGAGCTCTCACGGTCTGCACAGGACTGGCTGAT 978  
Db 1216 TACACAGCAGTACCGTGTGTGTGAGCTCTCACGGTCTGCACAGGACTGGCTGAT 1275  
Qy 979 GGCAGGAGTACAGTGCAGGTCTTCCAAAGAGCCCTCCAGCCCTCCATCAGAAACCC 1038  
Db 1276 GGCAGGAGTACAGTGCAGGTCTTCCAAAGAGCCCTCCAGCCCTCCATCAGAAACCC 1335  
Qy 1039 ATCTCAAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATCCCGG 1098  
Db 1336 ATCTCAAAGCCAAAGGGCAGCCCGAGAGAACCAAGGTGTACACCTGCCCCCATCCCGG 1395  
Qy 1099 GATGAGCTGACCAAGAACAGGTGAGCTGAGCTGCTGCTGCTCAAGGGCTTCTATCCAGC 1158  
Db 1396 GATGAGCTGACCAAGAACAGGTGAGCTGAGCTGCTGCTGCTCAAGGGCTTCTATCCAGC 1455  
Qy 1159 GACATCGCGTGGAGTGGAGAGCAATGGGAGCGCGAGAACCACTCAAGACCAACGCT 1218  
Db 1456 GACATCGCGTGGAGTGGAGAGCAATGGGAGCGCGAGAACCACTCAAGACCAACGCT 1515  
Qy 1219 CCGTGTGAGTCCGAGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1278  
Db 1516 CCGTGTGAGTCCGAGCGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1575  
Qy 1279 AGTGGCAGCAGGGNAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1338  
Db 1576 AGTGGCAGCAGGGNAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1635  
Qy 1339 TACAGCAGAGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1377  
Db 1636 TACAGCAGAGAGGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1674

RESULT 12  
ABQ74604

ID ABQ74604 standard; cDNA; 1674 BP.  
XX AC ABQ74604;  
XX DT 23-OCT-2002 (first entry)  
XX DE Mutation 1 Flt1(1-3 delta B)-Fc nucleotide sequence.  
XX KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
KW diabetic retinopathy; gene; ss.  
XX OS Homo sapiens.  
OS Synthetic.  
XX FH Key Location/Qualifiers  
XX FT CDS 1..1674  
XX FT /\*tag= a  
XX FT /product= "Mut1:Flt1(1-3 delta B)-Fc protein"  
XX PN WO200260489-A1.  
XX PD 08-AUG-2002.  
XX PF 28-JAN-2002; 2002WO-US002466.  
XX PR 31-JAN-2001; 2001US-00773877.  
XX PA (REGE-) REGENERON PHARM INC.  
XX PI Xia Y, Rudge JS, Yancopoulos GD;  
XX WPI; 2002-608488/65.  
XX P-PSDB; ABP52443.  
XX DR Treating psoriasis and enhancing wound healing in humans comprises the  
XX PT administration of a vascular endothelial cell growth factor (VEGF)  
XX PT antagonist.  
XX PS Example 11; Fig 13A-D; 179pp; English.  
XX CC The present invention describes a method for treating psoriasis and  
XX CC enhancing wound healing in a mammal or a human. The method comprises  
XX CC administering a vascular endothelial cell growth factor (VEGF) antagonist  
XX CC to the mammal or human. A VEGF antagonist has antipsoriatic,  
XX CC antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,  
XX CC nephrotropic and ophthalmological activities. The method can be used in  
XX CC treating psoriasis and enhancing wound healing in humans by administering  
XX CC VEGF antagonist. The method is also useful in treating clinical  
XX CC conditions characterised by vascular permeability, oedema or  
XX CC inflammation, such as brain oedema associated with injury, oedema  
XX CC associated with inflammatory disorders (e.g. rheumatoid arthritis),  
XX CC asthma, burns, kidney diseases, or eye disorders such as age-related  
XX CC macular degeneration and diabetic retinopathy. The method may also be  
XX CC used in making the polypeptide to decrease or inhibit plasma leakage and  
XX CC or vascular permeability. The present sequence encodes Mut1:Flt1(1-3  
XX CC delta B)-Fc which is used in an example from the present invention  
XX SQ Sequence 1674 BP; 495 A; 455 C; 378 G; 346 T; 0 U; 0 Other;  
Query Match 71.7%; Score 987.4; DB 6; Length 1674;  
Best Local Similarity 86.1%; Pred. No. 1.9e-229;  
Matches 1119; Conservative 0; Mismatches 171; Indels 9; Gaps 2;  
Qy 79 AGTGATCCGCTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATATACACATG 138  
Db 385 AGTGATCAGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATATACACATG 444  
Qy 139 ACTGAAGGAGGAGCTCGTCAATTCCTCCCTGCGGGTTACGTCACTCACTCACTGTTACT 198

Db 445 ACTGAAGGAGGAGCTCGTATTCCCTGCGGGTTACGTCACTTAACATCACTGTTACT 504  
Qy 199 TTAATAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAGAAACGATTAATCTGGGACAGT 258  
Db 505 TTAATAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAGAAACGATTAATCTGGGACAGT 564  
Qy 259 AGAAGGGCTTCATCATATCAAAATGAACGCTGACGAGTAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db 565 AGAAGGGCTTCATCATATCAAAATGAACGCTGACGAGTAAAGAAATAGGCTTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCAATTTGTATAAGACAAATCTCTCACATATCGACAAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCAATTTGTATAAGACAAATCTCTCACATATCGACAAACCAATACA 684  
Qy 379 ATCATAGATGGTTCGAGTCGGTCTCATGGAAATGGAATCTATCTGTGGAGAAAAGCTT 438  
Db 685 ATCATAGATGGTTCGAGTCGGTCTCATGGAAATGGAATCTATCTGTGGAGAAAAGCTT 744  
Qy 439 GTCTTAATTTACAGCAAGAACTGAACATAATGTGGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTTAATTTGACTGCTACCACTCCCTTGAAACGAGAGTTCAAAATGACCTGGAGTTAC 804  
Qy 499 CCTTCTTGAAGCATCAGCATAAGAAACTGTAAACCGAGACCTAAACCCAGTCTGGG 558  
Db 805 CCTGATGAATGTGACCAAGCAATCCCATGCCACATATTTCTACAGTGTCTTACTATT 864  
Qy 559 AGTGAGATGAAGAAATTTTGGACACCTTAATCTAGATGGTGTAAACCGGAGTGACCAA 618  
Db 865 GACAAATGCGAGAACAAAGACAAAGGACTTTATCTGTGCTGTAA--GGAAGTGGACCA 921  
Qy 619 GGAATGTACACTGTGAGCATCCAGTGGGCTGATGACCAAGAAACAGACACATTTGTC 678  
Db 922 TCATTCAAATCTGTTAACACCTC-----AGTGCATATATATGATAAAGCAGGCCCGGGC 975  
Qy 679 AGGATCCATGAAAGGACAAACTCACATATGCCCCGTCGCCAGACCTGAACTCTCTG 738  
Db 976 GAGCCAAATCTTGTGACAAACTCACATATGCCACCGTCCCGCAGCACTGAACTCTG 1035  
Qy 739 GGGAGACCGTCAGTCTTCTTCCCCCAAAACCCCAAGACACCTCATGATCTCCGG 798  
Db 1036 GGGGACCGTCAGTCTTCTTCCCCCAAAACCCCAAGACACCTCATGATCTCCGG 1095  
Qy 799 ACCCTGAGGTCAATGCGTGGTGTGAGTGCAGTGCAGCAAGACCCCTGAGGTCAAGTTC 858  
Db 1096 ACCCTGAGGTCAATGCGTGGTGTGAGTGCAGTGCAGCAAGACCCCTGAGGTCAAGTTC 1155  
Qy 859 AACTGGTACGTGGAGCGGTGAGTGCATTAATGCAAGACAAAGCCGCGGAGGAGCAG 918  
Db 1156 AACTGGTACGTGGAGCGGTGAGTGCATTAATGCAAGACAAAGCCGCGGAGGAGCAG 1215  
Qy 919 TACACAGCAGTACCGTGTGGTGTGAGTGTCTTCCAGTCTGACAGGACTGCTGAAT 978  
Db 1216 TACACAGCAGTACCGTGTGGTGTGAGTGTCTTCCAGTCTGACAGGACTGCTGAAT 1275  
Qy 979 GGCAGAGGTACAGTGCAGGTTCTTCAAAAGGCTTCCAGCCCTCCAGCCCATCGAAGAAC 1038  
Db 1276 GGCAGAGGTACAGTGCAGGTTCTTCAAAAGGCTTCCAGCCCTCCAGCCCATCGAAGAAC 1335  
Qy 1039 ATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCAGAGTGTACCCCTGCCCCATCCCGG 1098  
Db 1336 ATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCCAGAGTGTACCCCTGCCCCATCCCGG 1395  
Qy 1099 GATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGCTGTGCAAGGCTTCTATCCGAGC 1158  
Db 1396 GATGAGCTGACCAAGAACCCAGGTGAGCTGACCTGCTGTGCAAGGCTTCTATCCGAGC 1455  
Qy 1159 GACATCGCCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAACCAATCAAGACCAACGCT 1218  
Db 1456 GACATCGCCGTGGAGTGGGAGAGCAATGGGAGCGCGGAGAACCAATCAAGACCAACGCT 1515  
Qy 1219 CCGGTGTGAGTCCGAGCGCTCTTCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGC 1278

Db 1516 CCCGTGTGGACTCCGAGGCTCCTCTCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575  
Qy 1279 AGTGGCAGCAGAGGGAAACGTCTTCTCATGTCTCGTGTATGATGAGGCTCTGCACAAACAC 1338  
Db 1576 AGTGGCAGCAGAGGGAAACGTCTTCTCATGTCTCGTGTATGATGAGGCTCTGCACAAACAC 1635  
Qy 1339 TACACGCAAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1377  
Db 1636 TACACGCAAGAGAGCCCTCTCCCTGTCTCCGGGTAAATGA 1674  
RESULT 13  
AAA91073  
ID AAA91073 standard; DNA; 1704 BP.  
XX  
XX AAA91073;  
XX  
DT 05-APR-2001 (first entry)  
XX  
DE Flt1 receptor fusion protein Mut4:Flt1 (1-3R-N)-Fc coding sequence.  
XX  
XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
KW plasma leakage; vascular permeability; IgG Fc region; ss.  
XX  
XX Unidentified.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1704  
FT /\*tag= a  
FT /product= "Flt1(1-3R-N)-Fc"  
XX  
XX WO200075319-A1.  
XX  
XX 14-DEC-2000.  
XX  
XX 23-MAY-2000; 2000WO-US014142.  
XX  
XX 08-JUN-1999; 99US-0138133P.  
XX  
XX (REGE-) REGENERON PHARM INC.  
XX  
XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
XX WPI; 2001-071076/08.  
DR P-PSDB; AAY97593.  
XX  
XX Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems.  
XX  
XX Claim 9; Fig 16; 159pp; English.  
PS  
XX This sequence encodes a fusion protein of the invention between the Flt1  
XX receptor and the Fc region of IgG. The specification relates to modified  
XX chimeric polypeptides with improved pharmacokinetics. The modified  
XX chimeric polypeptides are preferably Flt1 receptor polypeptides that have  
XX been modified to improve their pharmacokinetic profile. The polypeptides  
XX can be used to decrease or inhibit plasma leakage and/or vascular  
XX permeability in a mammal  
XX  
SQ Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;  
Query Match 71.3%; Score 982.4; DB 5; Length 1704;  
Best Local Similarity 85.4%; Pred. No. 3.2e-228;  
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;  
Qy 79 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTTATACATG 138  
Db 385 AGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATCCCGAAATTTATACATG 444  
Qy 139 ACTGAAGGAGGAGGCTCGTCTTCTCCCTGCGGGTACGTCACCTAACATCACTGTTACT 198



Db 445 ACTGAAGGAGGAGCTCGTCATCTCCCTGCGGGTTACGTCACCTAACATCACTGTTACT 504  
Qy 199 TTAATAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAAAAACGATTAATCTGGACAGT 258  
Db 505 TTAATAAAGTTTCCACTTGACACTTTTGATCCCTGATGGAAAAACGATTAATCTGGACAGT 564  
Qy 259 AGAAGGGGTTTCATCATATCAAAATGCAAGGTAACAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db 565 AGAAGGGGTTTCATCATATCAAAATGCAAGGTAACAAAGAAATAGGCTTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCATTTGATAGACAAACTATCTCACATCGACCAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCATTTGATAGACAAACTATCTCACATCGACCAACCAATACA 684  
Qy 379 ATCATAGATGTGGTTCTGAGTCCGCTCATGGAATGAACTATCTGTTGGAGAAAAGCTT 438  
Db 685 ATCATAGATGTCAATTAAGCACACACCGCCAGTCAAAATTAATTTAGAGGCCATCTTT 744  
Qy 439 GTCTTAATTTGACAGCAAGAACTGAACTAAATGTGGGATTTGACTTCAACTTGGGAATAC 498  
Db 745 GTCTCAATTTGACTGCTACCACTCCCTTGAAACGAGAGTTCAAAATGACCTGGAGTTAC 804  
Qy 499 CTTCTTCGAGCATCAGCATAGAATCTGTAACCGGAGACCTTAAACCCAGTCTGGG 558  
Db 805 CTTGATGAAAAAATAAGAACGCTTCCGTAAGGCGACGAATTGACCAAGCAATTC---- 860  
Qy 559 AGTGAGATGAAGAAATTTTGAGCACCTTAACTATAGATGGTGTAAACCGGAGTGACCAA 618  
Db 861 --CCATGCCACATATTTCTACAGTGTCTTACTATTGCAAAATGCAAGCAAAAGACAAA 918  
Qy 619 GAATGTACACTGTGCGAGCATCCAGTGGGCTGATGACCAAGAAAGAACGACATTTGTC 678  
Db 919 GGACTTTATCTGTGCTGTAAGAGTGGACCATCATTTCAAATCTGTTAAACACCTCAGTG 978  
Qy 679 AGGTCCTATGAAA-----GGACAAACTCACACATGC 711  
Db 979 CATATATATGATAAAGACAGGCCGCGGCGAGCCCAAAATCTTGACAAAACCTCACATGC 1038  
Qy 712 CCACCGTGGCCAGCACCTGAACTCTCTGGGGAGCGCTCAGTCTTCTCTCCGCCCAAAA 771  
Db 1039 CCACCGTGGCCAGCACCTGAACTCTCTGGGGAGCGCTCAGTCTTCTCTCCGCCCAAAA 1098  
Qy 772 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGACGTG 831  
Db 1099 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGACGTG 1158  
Qy 832 AGCCAGGAGACCTTGAGGTCAAGTTCACTGTTAGTGGAGCGGCTGGAGGTGCAATAT 891  
Db 1159 AGCCAGGAGACCTTGAGGTCAAGTTCACTGTTAGTGGAGCGGCTGGAGGTGCAATAT 1218  
Qy 892 GCCAAGACAAAGCCGCGGAGGAGCAGTACACACGACGTACCGGTGCTGAGCGTCTC 951  
Db 1219 GCCAAGACAAAGCCGCGGAGGAGCAGTACACACGACGTACCGGTGCTGAGCGTCTC 1278  
Qy 952 ACCGTCTCCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCCAACAAA 1011  
Db 1279 ACCGTCTCCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCCAACAAA 1338  
Qy 1012 GCCCTCCACAGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCA 1071  
Db 1339 GCCCTCCACAGCCCATCGAAGAACCATCTCCAAAGCCAAAGGCGACCCCGGAGAACCA 1398  
Qy 1072 CAGGTGTACACCTCCGCCCATCCCGGATGAGCTGACCAAGAACCGAGTCAAGCTGACC 1131  
Db 1399 CAGGTGTACACCTCCGCCCATCCCGGATGAGCTGACCAAGAACCGAGTCAAGCTGACC 1458  
Qy 1132 TGCTGTGTCAAGGCTTCTATCCACAGCGACATCGCGGTGGAGTGGGAGCAATGGGCGAG 1191  
Db 1459 TGCTGTGTCAAGGCTTCTATCCACAGCGACATCGCGGTGGAGTGGGAGCAATGGGCGAG 1518  
Qy 1192 CCGGAGAACATACAGACACCGCTCCGCTGCTGGAATCCGAGCGGTCTCTTCTTCTC 1251  
Db 1519 CCGGAGAACATACAGACACCGCTCCGCTGCTGGAATCCGAGCGGTCTCTTCTTCTC 1578

Qy 1252 TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGAGGGGAAAGCTTCTTCATGCTCC 1311  
Db 1579 TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGAGGGGAAAGCTTCTTCATGCTCC 1638  
Qy 1312 GTGATGATGAGGCTCTGCAACAACATACACGAGAGAGCCTTCCCTGTCTCCGGGT 1371  
Db 1639 GTGATGATGAGGCTCTGCAACAACATACACGAGAGAGCCTTCCCTGTCTCCGGGT 1698  
Qy 1372 AAATGA 1377  
Db 1699 AAATGA 1704

## RESULT 14

ABQ74607  
ID ABQ74607 standard; cDNA; 1704 BP.  
XX  
AC ABQ74607;  
XX  
DT 23-OCT-2002 (first entry)  
XX  
DE Mutation 4 Flt1(2-3 R-N)-Fc nucleotide sequence.  
XX  
KW Human; Flt1; vascular endothelial growth factor; VEGF; VEGF antagonist;  
KW psoriasis; wound healing; Flt1 receptor; antipsoriatic; antiinflammatory;  
KW vulnery; antiasthmatic; antirheumatic; antiarthritic; nephrotropic;  
KW ophthalmological; vascular permeability; oedema; inflammation; asthma;  
KW brain oedema; inflammatory disorder; rheumatoid arthritis; burn;  
KW kidney disease; eye disorder; age-related macular degeneration;  
XX diabetic retinopathy; gene; ss.  
OS Homo sapiens.  
XX Synthetic.  
FH Key  
FT CDS  
FT Location/Qualifiers  
FT 1..1704  
FT /\*tag= a  
FT /product= "Mut4:Flt1(2-3 R-N)-Fc protein"  
XX  
XX WO200260489-A1.  
XX  
XX 08-AUG-2002.  
XX  
XX 28-JAN-2002; 2002WO-US002466.  
XX  
XX 31-JAN-2001; 2001US-00773877.  
XX  
XX (REGG-) REGENERON PHARM INC.  
XX  
XX Xia Y, Rudge JS, Yancopoulos GD;  
XX  
XX WPI; 2002-608488/65.  
XX  
XX P-ESDB; ABP52446.  
XX  
XX Treating psoriasis and enhancing wound healing in humans comprises the  
XX administration of a vascular endothelial cell growth factor (VEGF)  
XX antagonist.  
XX  
XX Example 14; Fig 16A-D; 179pp; English.  
XX  
XX The present invention describes a method for treating psoriasis and  
XX enhancing wound healing in a mammal or a human. The method comprises  
XX administering a vascular endothelial cell growth factor (VEGF) antagonist  
XX to the mammal or human. A VEGF antagonist has antipsoriatic,  
XX antiinflammatory, vulnery, antiasthmatic, antirheumatic, antiarthritic,  
XX nephrotropic and ophthalmological activities. The method can be used in  
XX treating psoriasis and enhancing wound healing in humans by administering  
XX VEGF antagonist. The method is also useful in treating clinical  
XX conditions characterised by vascular permeability, oedema or  
XX inflammation, such as brain oedema associated with injury, oedema  
XX associated with inflammatory disorders (e.g. rheumatoid arthritis),  
XX asthma, burns, kidney diseases, or eye disorders such as age-related

CC macular degeneration and diabetic retinopathy. The method may also be  
CC used in making the polypeptide to decrease or inhibit plasma leakage and  
CC or vascular permeability. The present sequence encodes Mut4:Flt1(2-3 R-  
XX >N)-Fc which is used in an example from the present invention  
SQ Sequence 1704 BP; 508 A; 461 C; 385 G; 350 T; 0 U; 0 Other;

Query Match 71.3%; Score 982.4; DB 6; Length 1704;  
Best Local Similarity 85.4%; Pred. No. 3.2e-228;  
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;

Qy 79 AGTGATACCGGTAGACCTTTTCGTAGAGATGATACAGTGAATCCCGAAATTTATACACATG 138  
Db |||||  
Qy 385 AGTGATACAGGTAGACCTTTTCGTAGAGATGATACAGTGAATCCCGAAATTTATACACATG 444  
Db |||||  
Qy 139 ACTGAAGGAAGGAGCTCGTCAATCCCTGCCGGTTACGTCAACCTAACATCACTGTTACT 198  
Db |||||  
Qy 445 ACTGAAGGAAGGAGCTCGTCAATCCCTGCCGGTTACGTCAACCTAACATCACTGTTACT 504  
Db |||||  
Qy 199 TTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAAACGATATCTGGACAGT 258  
Db |||||  
Qy 505 TTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAAAACGATATCTGGACAGT 564  
Db |||||  
Qy 259 AGAAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db |||||  
Qy 565 AGAAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGCTTCTGACCTGTGAA 624  
Db |||||  
Qy 319 GCAACAGTCAATGGGCATTTGTATAAGACAAATATCTCACACATCGAACAAACCAATACA 378  
Db |||||  
Qy 625 GCAACAGTCAATGGGCATTTGTATAAGACAAATATCTCACACATCGAACAAACCAATACA 684  
Db |||||  
Qy 379 ATCATAGATGGTTCGTAGTCCGCTCTCATGGATTGAACTATCTGTTGGAGAAAGCTT 438  
Db |||||  
Qy 685 ATCATAGATGGTTCGTAGTCCGCTCTCATGGATTGAACTATCTGTTGGAGAAAGCTT 744  
Db |||||  
Qy 439 GTCCTTAAATTTGTACAGCAAGCACTGAATAATGTGGGGATTGACTTCAACTGGGAATAC 498  
Db |||||  
Qy 745 GTCCCTAATGTACTGCTACCACTCCCTTGAACACGAGAGTTCAANTGACCTGAGTTAC 804  
Db |||||  
Qy 499 CTTCTTCGAGAGCATACGATACGATGAACTTTGTAAACCGAGACCTTAAACCCAGTGTGG 558  
Db |||||  
Qy 805 CTTGATGAAAAAATAAGAACGCTTCCGTAAGGCGACGAATTTGACCAAGCAATTC--- 860  
Db |||||  
Qy 559 AGTGAGATGAAAGAAATTTTTCGACACCTTAAGTATAGTGTGTAAACCGAGTGCACAA 618  
Db |||||  
Qy 861 ---CCATGCCACATATTTACAGTGTCTTACTATTGACAAATGCGAAACAAAGACAAA 918  
Db |||||  
Qy 619 GGATTTGACACTGTGACGATCCAGTGGGCTGATGACCAAGAAAGAACAGCACATTTGTC 678  
Db |||||  
Qy 919 GGACTTTATATCTGTCGTGTAAGGATGACCATCATTCNAATCTGTTAACACCTCAGTG 978  
Db |||||  
Qy 679 AGGTGTCATGAAA-----GGACAAACTTCACACATGC 711  
Db |||||  
Qy 979 CATATATATATAAGACAGCGCCGGCGAGCCCAAAATCTTGTGACAAAACTTCACACATGC 1038  
Db |||||  
Qy 712 CCACGTCGCCGACACCTGAACTCTGGGGGACGCTCTTCCTCTCCCGCCCAAAA 771  
Db |||||  
Qy 1039 CCACGTCGCCGACACCTGAACTCTGGGGGACGCTCTTCCTCTCCCGCCCAAAA 1098  
Db |||||  
Qy 772 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGACGTG 831  
Db |||||  
Qy 1099 CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGACGTG 1158  
Db |||||  
Qy 832 AGCCACGAAGACCTGTAGGTCAAGTTCAATGTTGATCGTGGACCGGTGGAGGTGCAATAT 891  
Db |||||  
Qy 1159 AGCCACGAAGACCTGTAGGTCAAGTTCAATGTTGATCGTGGACCGGTGGAGGTGCAATAT 1218  
Db |||||  
Qy 892 GCCAAGACAAAGCCGCGGAGGACGATACACAGCAGTACCGTGGTGGTGGTGGTGGTGGT 951  
Db |||||  
Qy 1219 GCCAAGACAAAGCCGCGGAGGACGATACACAGCAGTACCGTGGTGGTGGTGGTGGTGGT 1278  
Db |||||  
Qy 952 ACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCACAAA 1011  
Db |||||

Db 1279 ACCGTCTCTGCACAGGACTGGCTGAATGGCAAGGAGTACAAGTGCRAAGGTCTCCACAAA 1338  
Qy 1012 GCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGGAGGCCCGGAGAACCA 1071  
Db |||||  
Qy 1339 GCCCTCCAGCCCCCATCGAGAAAAACCATCTCCAAAGCCAAAGGGGAGGCCCGGAGAACCA 1398  
Db |||||  
Qy 1072 CAGGTGTACACCCCTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTGACGCTGACC 1131  
Db |||||  
Qy 1399 CAGGTGTACACCCCTGCCCCCATCCCGGGATGAGTGAACCAAGAACCAAGGTGACGCTGACC 1458  
Db |||||  
Qy 1132 TGCCTGTCAAAGGCTTCTATCCAGCGACATCGCCCTGGAGTGGAGAGCAATGGGCAG 1191  
Db |||||  
Qy 1459 TGCCTGTCAAAGGCTTCTATCCAGCGACATCGCCCTGGAGTGGAGAGCAATGGGCAG 1518  
Db |||||  
Qy 1192 CCGGAGAAACAACTAACAGACACGCTCCCGTCCGCTGAGTCCCGACGGCTCTTCTTCTC 1251  
Db |||||  
Qy 1519 CCGGAGAAACAACTAACAGACACGCTCCCGTCCGCTGAGTCCCGACGGCTCTTCTTCTC 1578  
Db |||||  
Qy 1252 TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGACGCTTCTCATGCTCC 1311  
Db |||||  
Qy 1579 TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGACGCTTCTCATGCTCC 1638  
Db |||||  
Qy 1312 GTGATGATGAGGCTCTGACAAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCCGGT 1371  
Db |||||  
Qy 1639 GTGATGATGAGGCTCTGACAAACCACTACACGCAAGAGCCCTCTCCCTGTCTCCCGGT 1698  
Db |||||  
Qy 1372 AAATGA 1377  
Db |||||  
Qy 1699 AAATGA 1704  
Db |||||

RESULT 15  
AAA91077  
ID AAA91077 standard; DNA; 1704 BP.  
XX  
XX AAA91077;  
XX AC  
XX AC  
DT 05-APR-2001 (first entry)  
XX  
DE Flt1 receptor protein Flt1(1-3)-Fc coding sequence.  
XX  
XX Flt1 receptor; fusion protein; chimeric protein; pharmacokinetic;  
KW plasma leakage; vascular permeability; IgG Fc region; ss.  
XX  
OS Unidentified.  
XX  
FH Key Location/Qualifiers  
CDS 1..1704  
FT /\*tag= a  
FT /product= "Flt1(1-3)-Fc"  
XX  
XX W020075319-Al.  
FN  
XX  
XX 14-DEC-2000.  
XX  
XX 23-MAY-2000; 2000WO-US014142.  
PP  
XX  
XX 08-JUN-1999; 99US-0138133P.  
PR  
XX (REGE-) REGENERON PHARM INC.  
PA  
XX Papadopoulos NJ, Davis S, Yancopoulos GD;  
XX  
XX WPI; 2001-071076/08.  
DR  
XX P-PSDB; AAY97597.  
XX  
PT Nucleic acid molecule encoding mammalian phospholipid transfer protein,  
PT and its fragments, useful for diagnosis, evaluation, and treatment of  
PT diseases associated with the gene expression and for producing model  
PT systems.  
XX  
XX Example 11; Fig 10; 159pp; English.  
XX



**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 21:19:06 ; Search time 4869.12 Seconds  
(without alignments)  
10764.685 Million cell updates/sec

Title: US-10-009-852-15  
Perfect score: 1377  
Sequence: 1 atggtcagctactgggacac.....ccctgtctccgggtaaatga 1377

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	684	49.7	871	4 BG753979	602709506
2	684	49.7	983	5 BQ708975	BQ708975 AGENCOURT
3	683	49.6	941	5 BQ712021	BQ712021 AGENCOURT
4	682.4	49.6	843	4 BM007897	BM007897 603617582
5	682.4	49.6	925	5 BQ709152	BQ709152 AGENCOURT
6	682.4	49.6	1022	3 CR611254	CR611254 full-leng
7	682.4	49.6	1048	3 CR595172	CR595172 full-leng
8	682.4	49.6	1090	3 CR612308	CR612308 full-leng
9	682.4	49.6	1091	3 CR604961	CR604961 full-leng
10	682.4	49.6	1093	3 CR616804	CR616804 full-leng
11	682.4	49.6	1098	3 CR626477	CR626477 full-leng
12	682.4	49.6	1100	3 CR612813	CR612813 full-leng
13	682.4	49.6	1102	3 CR601777	CR601777 full-leng
14	682.4	49.6	1102	3 CR625051	CR625051 full-leng
15	682.4	49.6	1103	3 CR595194	CR595194 full-leng
16	682.4	49.6	1104	3 CR591904	CR591904 full-leng
17	682.4	49.6	1106	3 CR613460	CR613460 full-leng
18	682.4	49.6	1106	3 CR620071	CR620071 full-leng
19	682.4	49.6	1107	3 CR598548	CR598548 full-leng
20	682.4	49.6	1109	3 CR614200	CR614200 full-leng
21	682.4	49.6	1109	3 CR619687	CR619687 full-leng
22	682.4	49.6	1111	3 CR606782	CR606782 full-leng
23	682.4	49.6	1114	3 CR593349	CR593349 full-leng
24	682.4	49.6	1114	3 CR618075	CR618075 full-leng

ALIGNMENTS

RESULT 1  
BG753979 602709506F1 NIH\_MGC\_48 Homo sapiens CDNA clone IMAGE:4846201 5',  
LOCUS mRNA sequence.  
DEFINITION BG753979.1 GI:14064632  
ACCESSION BG753979  
VERSION EST.  
KEYWORDS Homo sapiens (human)  
SOURCE EST.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 871)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
Plate: LICM1686 row: k column: 02  
High quality sequence stop: 848.  
Location/Qualifiers  
1. 871  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4846201"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC 48"  
/note="Organ: B-cells; Vector: pOTB7; Site:1: XhoI; Site:2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

FEATURES  
source

ORIGIN

Query Match 49.7%; Score 684; DB 4; Length 871;  
Best Local Similarity 100.0%; Pred. No. 4.7e-179; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCCGTGGCCAGCACCCTCATGATCTCCGGAGCCCTGAGGTCA 753  
DB 37 GACAAACTCACATGCCCGTGGCCAGCACCCTGAACCTCTTGGGGGACCGTCAGTC 96

QY 754 TTCTCTTTCCCGCCAAACCCAGAGACACCCTCATGATCTCCGGAGCCCTGAGGTCA 813  
DB 97 TTCTCTTTCCCGCCAAACCCAGAGACACCCTCATGATCTCCCGGACCCCTGAGGTCA 156

QY 814 TGCGTGGTGGAGCTGAGCAGCAGCAGCAGCCTGAGGTCAAGTTCACCTGCTAGCTGAC 873  
DB 157 TGCGTGGTGGAGCTGAGCAGCAGCAGCAGCCTGAGGTCAAGTTCACCTGCTAGCTGAC 216

QY 874 GCGGTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAAACAGCACGTCAC 933  
DB 217 GCGGTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAAACAGCACGTCAC 276

QY 934 CGTGTGGTCAAGGTCTCACCCTGCTGACAGAGACTGGCTGAATGGCAAGAGGTACAG 993  
DB 277 CGTGTGGTCAAGGTCTCACCCTGCTGACAGAGACTGGCTGAATGGCAAGAGGTACAG 336

QY 994 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAA 1053  
DB 337 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAA 396

QY 1054 GCGCAGCCCCGAGAACCAAGGTGTACACCTCGCCCATCCCGGGATGAGCTGACCAAG 1113  
DB 397 GCGCAGCCCCGAGAACCAAGGTGTACACCTCGCCCATCCCGGGATGAGCTGACCAAG 456

QY 1114 AACCAAGTCAAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173  
DB 457 AACCAAGTCAAGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 516

QY 1174 TGGGAGAGCAATGGGACGCGGAGAACCAACTACAGACCCAGCTCCCGTCTGAGCTCC 1233  
DB 517 TGGGAGAGCAATGGGACGCGGAGAACCAACTACAGACCCAGCTCCCGTCTGAGCTCC 576

QY 1234 GACGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGG 1293  
DB 577 GACGCTCTCTTCTCTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGG 636

QY 1294 AACGCT 1353  
DB 637 AACGCT 696

QY 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377  
DB 697 CTCTCCCTGTCTCCGGGTAAATGA 720

RESULT 2  
LOCUS BQ708975  
DEFINITION BQ708975 983 bp mRNA linear EST 16-JUL-2002  
5', mRNA sequence.  
ACCESSION BQ708975  
VERSION BQ708975.1 GI:21847874  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 983)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Dr. Mark Watson  
CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLCM2469 row: k column: 12  
High quality sequence stop: 604.  
Location/Qualifiers  
1. .983  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="INAGB:6279683"  
/lab\_host="NIH\_MGC\_113"  
/lab\_host="DH10B (phage-resistant)"  
/notes="Organ: spleen; Vector: pOTB7; Site: 1: XhoI; Site 2:  
EcoRI; CDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 49.7%; Score 684; DB 5; Length 983;  
Best Local Similarity 100.0%; Pred. No. 4.9e-179; Indels 0; Gaps 0;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCCGTGGCCAGCACCCTGAACCTCTCCGGGGACCGTCAGTC 753  
DB 24 GACAAACTCACATGCCCGTGGCCAGCACCCTGAACCTCTCCGGGGACCGTCAGTC 83

QY 754 TTCTCTTTCCCGCCAAACCCAGGACACCCTCATGATCTCCGGGACCCCTGAGGTCA 813  
DB 84 TTCTCTTTCCCGCCAAACCCAGGACACCCTCATGATCTCCGGGACCCCTGAGGTCA 143

QY 814 TGCGTGGTGGAGCTGAGCAGCAGCAGCAGCCTGAGGTCAAGTTCACCTGCTGAGTCC 873  
DB 144 TGCGTGGTGGAGCTGAGCAGCAGCAGCAGCCTGAGGTCAAGTTCACCTGCTGAGTCC 203

QY 874 GCGGTGAGGTGTCATAATGCCAAGAACCGCGGGAGGAGCAGTACAAACAGCACCGTAC 933  
DB 204 GCGGTGAGGTGTCATAATGCCAAGAACCGCGGGAGGAGCAGTACAAACAGCACCGTAC 263

QY 934 CGTGTGTGAGCTGCTCTCACCGCTCTGCAACAGGACTGGCTGTAATGGCAAGAGGTACA 993  
DB 264 CGTGTGTGAGCTGCTCTCACCGCTCTGCAACAGGACTGGCTGTAATGGCAAGAGGTACA 323

QY 994 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAA 1053  
DB 324 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAACCATCTCCAAAGCCAAA 383

QY 1054 GGGCAGCCCCGAGAACCAACAGGTGTACACCTCGCCGCCCATCCCGGGATGAGCTGACCAAG 1113  
DB 384 GGGCAGCCCCGAGAACCAACAGGTGTACACCTCGCCGCCCATCCCGGGATGAGCTGACCAAG 443

QY 1114 AACCAAGTCAAGCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173  
DB 444 AACCAAGTCAAGCTGAGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 503

QY 1174 TGGGAGAGCAATGGGACGCGGAGAACCAACTACAGACCCAGCTCCCGTCTGAGCTCC 1233  
DB 504 TGGGAGAGCAATGGGACGCGGAGAACCAACTACAGACCCAGCTCCCGTCTGAGCTCC 563

QY 1234 GACGCTCTCTTCT 1293  
DB 564 GACGCTCTCTTCT 623

QY 1294 AACGCT 1353  
DB 624 AACGCT 683

```
QY 1354 CTCTCCCTGCTCTCCGGTAAATGA 1377
Db 684 CTCTCCCTGCTCTCCGGTAAATGA 707

RESULT 3
BQ712021
LOCUS BQ712021 941 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8418162 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281403
5', mRNA sequence.
ACCESSION BQ712021
VERSION BQ712021
KEYWORDS BQ712021.1 GI:21850920
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 941)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2474 row: c column: 04
High quality sequence stop: 638.
Location/Qualifiers
1. 941
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6281403"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
```

```
QY 994 TGCAGGCTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA 1053
Db 350 TGCAGGCTCTCAACAAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA 409

1054 GGGCAGCCCCCAGAAACCAAGGTGTACACCTGCGCCCCCATCCCGGATGAGCTGACCAAG 1113
Db 410 GGGCAGCCCCCAGAAACCAAGGTGTACACCTGCGCCCCCATCCCGGATGAGCTGACCAAG 469

1114 AACAGGTCAGCCTGACCTGCTGGTCAAGGGCTTCTATCCAGCGCATCGCCGTGGAG 1173
Db 470 AACAGGTCAGCCTGACCTGCTGGTCAAGGGCTTCTATCCAGCGCATCGCCGTGGAG 529

1174 TGGGAGAGCAATGGCAGCCGAGAAACATACAGACACGCGCTCCCGTGTGACTCC 1233
Db 530 TGGGAGAGCAATGGCAGCCGAGAAACATACAGACACGCGCTCCCGTGTGACTCC 589

1234 GACGGCTCTTTCTTCTCTACAGCAAGCTACCGTGGCAAGAGCAGGTGGCAGCAGGG 1293
Db 590 GACGGCTCTTTCTTCTCTACAGCAAGCTACCGTGGCAAGAGCAGGTGGCAGCAGGG 649

1294 AACGCTCTCTCATGCTCGTGATGCATGAGGCTCTGCACACCACTACACGAGAGGC 1353
Db 650 AACGCTCTCTCATGCTCGTGATGCATGAGGCTCTGCACACCACTACACGAGAGGC 709

1354 CTCTCCCTGCTCTCCGGTAAATGA 1377
Db 710 CTCTCCCTGCTCTCCGGTAAATGA 733

RESULT 4
BQ007897
LOCUS BQ007897 843 bp mRNA linear EST 30-OCT-2001
DEFINITION 603617582P1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450469 5',
mRNA sequence.
ACCESSION BQ007897
VERSION BQ007897
KEYWORDS BQ007897.1 GI:16522238
SOURCE EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 843)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1939 row: d column: 22
High quality sequence stop: 833.
Location/Qualifiers
1. 843
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5450469"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site:1: XhoI; Site:2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
```

```
QY 694 GACAAACTCACATGCCACCGTCCAGCACCCTGAACTCTGGGGGACCGTCAGTC 753
Db 50 GACAAACTCACATGCCACCGTCCAGCACCCTGAACTCTGGGGGACCGTCAGTC 109

754 TTCTCTTCCCCCAAAACCCAGACACCTCATGATCTCCGAGACCCCTGAGGTACA 813
Db 110 TTCTCTTCCCCCAAAACCCAGACACCTCATGATCTCCGAGACCCCTGAGGTACA 169

814 TGCGTGGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
Db 170 TGCGTGGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

874 GCGGTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAACAGCACGTAC 933
Db 230 GCGGTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAACAGCACGTAC 289

934 CGTGTGGTCAGGCTCCTCAGCGTCTGACAGGACTGGCTGAATGGCAAGGATACAAG 993
Db 290 CGTGTGGTCAGGCTCCTCAGCGTCTGACAGGACTGGCTGAATGGCAAGGATACAAG 349
```

```
ORIGIN
Query Match 49.6%; Score 683; DB 5; Length 941;
Best Local Similarity 99.9%; Pred. No. 9,2e-179;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCACCGTCCAGCACCCTGAACTCTGGGGGACCGTCAGTC 753
Db 50 GACAAACTCACATGCCACCGTCCAGCACCCTGAACTCTGGGGGACCGTCAGTC 109

QY 754 TTCTCTTCCCCCAAAACCCAGACACCTCATGATCTCCGAGACCCCTGAGGTACA 813
Db 110 TTCTCTTCCCCCAAAACCCAGACACCTCATGATCTCCGAGACCCCTGAGGTACA 169

QY 814 TGCGTGGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
Db 170 TGCGTGGTGGAGCTGAGCCAGACACCTGAGGTCAAGTTCAACTGGTACGTGGAC 229

QY 874 GCGGTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAACAGCACGTAC 933
Db 230 GCGGTGGAGGTGCATAATGCCAAGAACCGCGGGAGGAGCAGTACAACAGCACGTAC 289

QY 934 CGTGTGGTCAGGCTCCTCAGCGTCTGACAGGACTGGCTGAATGGCAAGGATACAAG 993
Db 290 CGTGTGGTCAGGCTCCTCAGCGTCTGACAGGACTGGCTGAATGGCAAGGATACAAG 349
```



ORIGIN

Query Match 49.6%; Score 682.4; DB 4; Length 843;  
Best Local Similarity 99.9%; Pred. No. 1.3e-178;  
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 694 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTCTGGGGGACCGTCAAGTC 753  
Db 108 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTCTGGGGGACCGTCAAGTC 167

Qy 754 TTCCTCTTCCCTCCCAAAACCAAGGACACCTCTCATGATCTCCCGGACCCCTTGAGGTCAACA 813  
Db 168 TTCCTCTTCCCTCCCAAAACCAAGGACACCTCTCATGATCTCCCGGACCCCTTGAGGTCAACA 227

Qy 814 TGCCTGTGTGGAGCTGAGCCAGACGACCTCTGAGGTCAAGTTCAACTGTTGAGTGGAC 873  
Db 228 TGCCTGTGTGGAGCTGAGCCAGACGACCTCTGAGGTCAAGTTCAACTGTTGAGTGGAC 287

Qy 874 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCACGTAC 933  
Db 288 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCACGTAC 347

Qy 934 CGTGTGTGTGAGCTCTCACCGTCTGACCCAGGACTGGCTGAATGGCAAGGAGTACAAG 993  
Db 348 CGTGTGTGTGAGCTCTCACCGTCTGACCCAGGACTGGCTGAATGGCAAGGAGTACAAG 407

Qy 994 TGCAGAGTCTCAACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAA 1053  
Db 408 TGCAGAGTCTCAACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAA 467

Qy 1054 GGGCAGCCCGCAGAACACAGGTGTACACCTCTGCCCTCCCTATCCAGCGACATCGCCGTGGAG 1113  
Db 468 GGGCAGCCCGCAGAACACAGGTGTACACCTCTGCCCTCCCTATCCAGCGACATCGCCGTGGAG 527

Qy 1114 AACGAGTTCAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCCGTGGAG 1173  
Db 528 AACGAGTTCAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCCGTGGAG 587

Qy 1174 TGGAGAGCAATGGGAGCCGGAGAACAACTACAAAGACCGCTCTCCGCTGGAGTCC 1233  
Db 588 TGGAGAGCAATGGGAGCCGGAGAACAACTACAAAGACCGCTCTCCGCTGGAGTCC 647

Qy 1234 GACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAGAGCAGTGGCAGCAGGG 1293  
Db 648 GACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAGAGCAGTGGCAGCAGGG 707

Qy 1294 AACCTCTTCTCATGCTCCGTCATGAGGCTCTGCACACACCTACACGCAAGAGC 1353  
Db 708 AACCTCTTCTCATGCTCCGTCATGAGGCTCTGCACACACCTACACGCAAGAGC 767

Qy 1354 CTCTCTCTGCTCCGGGTAAATGA 1377  
Db 768 CTCTCTCTGCTCCGGGTAAATGA 791

RESULT 5  
BQ709152  
LOCUS  
DEFINITION BQ709152 925 bp mRNA linear EST 16-JUL-2002  
5', mRNA sequence.  
ACCESSION BQ709152  
VERSION BQ709152.1 GI:21848051  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 925)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson  
cDNA Library Preparation: Rubin Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LCM2516 row: m column: 22  
High quality sequence stop: 739.

FEATURES

source 1. .925  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6301245"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_113"  
/notes="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

ORIGIN

Query Match 49.6%; Score 682.4; DB 5; Length 925;  
Best Local Similarity 99.9%; Pred. No. 1.3e-178;  
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 694 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTGGGGGACCGTCAAGTC 753  
Db 48 GACAAACTCACATGCTCCACCGTGGCCAGCAGCTGAACCTCTGGGGGACCGTCAAGTC 107

Qy 754 TTCCTCTTCCCTCCCAAAACCAAGGACACCTCTCATGATCTCCCGGACCCCTTGAGGTCAACA 813  
Db 108 TTCCTCTTCCCTCCCAAAACCAAGGACACCTCTCATGATCTCCCGGACCCCTTGAGGTCAACA 167

Qy 814 TGCCTGTGTGAGCTGAGCCAGACGACCTCTGAGGTCAAGTTCAACTGTTGAGTGGAC 873  
Db 168 TGCCTGTGTGAGCTGAGCCAGACGACCTCTGAGGTCAAGTTCAACTGTTGAGTGGAC 227

Qy 874 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCACGTAC 933  
Db 228 GGCCTGTGGAGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAGTACACAGCACGTAC 287

Qy 934 CGTGTGTGTGAGCTCTCACCGTCTGACCCAGGACTGGCTGAATGGCAAGGAGTACAAG 993  
Db 288 CGTGTGTGTGAGCTCTCACCGTCTGACCCAGGACTGGCTGAATGGCAAGGAGTACAAG 347

Qy 994 TGCAGAGTCTCAACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAA 1053  
Db 348 TGCAGAGTCTCAACAAAGCCCTCCAGCCCTCCATCGAGAAACCATCTCCAAAGCCAAA 407

Qy 1054 GGGCAGCCCGCAGAACACAGGTGTACACCTCTGCCCTCCCTATCCAGCGACATCGCCGTGGAG 1113  
Db 408 GGGCAGCCCGCAGAACACAGGTGTACACCTCTGCCCTCCCTATCCAGCGACATCGCCGTGGAG 467

Qy 1114 AACGAGTTCAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCCGTGGAG 1173  
Db 468 AACGAGTTCAGCTGACCTGCTGCTCAAGAGCTTCTATCCAGCGACATCGCCGTGGAG 527

Qy 1174 TGGAGAGCAATGGGAGCCGGAGAACAACTACAAAGACCGCTCTCCGCTGGAGTCC 1233  
Db 528 TGGAGAGCAATGGGAGCCGGAGAACAACTACAAAGACCGCTCTCCGCTGGAGTCC 587

Qy 1234 GACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAGAGCAGTGGCAGCAGGG 1293  
Db 588 GACGGCTCTTCTTCTCTACAGCAAGCTACCGTGGACAGAGCAGTGGCAGCAGGG 647

Qy 1294 AACCTCTTCTCATGCTCCGTCATGAGGCTCTGCACACACCTACACGCAAGAGC 1353  
Db 708 AACCTCTTCTCATGCTCCGTCATGAGGCTCTGCACACACCTACACGCAAGAGC 1353

```
Db      648 AACGCTTCTCANGCTCCGTGATGATGAGGCTCTGCACAACCACTACACAGAGAAGC 707
Qy      1354 CTCTCCCTGCTCCGGGTAATGA 1377
Db      708 CTCTCCCTGCTCCGGGTAATGA 731

RESULT 6
LOCUS   CR611254              1022 bp      mRNA      linear      HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DE007YJ17 of Placenta of Homo sapiens (human).
ACCESSION CR611254
VERSION   CR611254.1 GI:50492061
KEYWORDS HTC; CNSLT cDNA.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1022)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 1022)
REFERENCE Genoscope.
AUTHORS   Direct Submission
TITLE     Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL   BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
FEATURES   Location/Qualifiers
source     1..1022
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DE007YJ17"
            /tissue_type="Placenta"
            /plasmid="pCMVSPORT_6"

ORIGIN
Query Match 49.6%; Score 682.4; DB 3; Length 1022;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      694 GACAAAACCTCACATGCCACCGTCCGAGCACTGAACTCCTGGGGGACCGTCAGTC 753
Db      323 GACAAAACCTCACATGCCACCGTCCGAGCACTGAACTCCTGGGGGACCGTCAGTC 382
Qy      754 TTCTCTTTCCCCCAAAACCAAGACACCTCATGATCTCCGAGCCCTTGAGGTACA 813
Db      383 TTCTCTTTCCCCCAAAACCAAGACACCTCATGATCTCCGAGCCCTTGAGGTACA 442
Qy      814 TGGTGGTGGTGGAGCGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTAGCTGGAC 873
Db      443 TGGTGGTGGTGGAGCGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTAGCTGGAC 502
Qy      874 GGGTGGAGGTGCATAAATGCCNAGCAAAGCGCGGAGGAGCAGTACAACAGACGCTAC 933
Db      503 GCGGTGGAGGTGCATAAATGCCNAGCAAAGCGCGGAGGAGCAGTACAACAGACGCTAC 562
Qy      934 CGTGGGTGAGGTCTCTCACCGTCTCTGCACAGGACTGGCTGAATGGCAAGAGTACAAG 993
Db      563 CGTGGGTGAGGTCTCTCACCGTCTCTGCACAGGACTGGCTGAATGGCAAGAGTACAAG 622
Qy      994 TGCAGAGTCTCCAAACAAAGCCCTCCACGCCCCCAATCGAGAAACCACTCTCCAAAGCCAAA 1053
          |||||||
```

```
Db      623 TGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATCGAGAAAACCACTCTCCAAAGCCAAA 682
Qy      1054 GGGCAGCCCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1113
Db      683 GGGCAGCCCCCGAGAACACACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 742
Qy      1114 AACCAGGTTCAGCTGACCTGCTGGTCAAAAGGCTTTCTATCCAGCGACATCGCGTGGAG 1173
Db      743 AACCAGGTTCAGCTGACCTGCTGGTCAAAAGGCTTTCTATCCAGCGACATCGCGTGGAG 802
Qy      1174 TGGGAGAGCAATGGGAGCCCGAGAGAACTACAGACCAAGCTCCCGTCTGCTGACTCC 1233
Db      803 TGGGAGAGCAATGGGAGCCCGAGAGAACTACAGACCAAGCTCCCGTCTGCTGACTCC 862
Qy      1234 GACGCTCTCTTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGCAGCAGGG 1293
Db      863 GACGCTCTCTTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGCAGCAGGG 922
Qy      1294 AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACACGAGAAGAGC 1353
Db      923 AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAACCACTACACGAGAAGAGC 982
Qy      1354 CTCTCCCTGTCTCCGGGTAATGA 1377
Db      983 CTCTCCCTGTCTCCGGGTAATGA 1006

RESULT 7
LOCUS   CR595172              1048 bp      mRNA      linear      HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI040YA16 of Placenta Cot 25-normalized
          of Homo sapiens (human).
ACCESSION CR595172
VERSION   CR595172.1 GI:50475979
KEYWORDS HTC; CNSLT cDNA.
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1048)
AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE     Full-length cDNA libraries and normalization
JOURNAL   Unpublished
REMARK    Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 1048)
REFERENCE Genoscope.
AUTHORS   Direct Submission
TITLE     Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
JOURNAL   BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
COMMENT   1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
FEATURES   Location/Qualifiers
source     1..1048
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CS0DI040YA16"
            /tissue_type="Placenta Cot 25-normalized"
            /plasmid="pCMVSPORT_6"

ORIGIN
Query Match 49.6%; Score 682.4; DB 3; Length 1048;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      694 GACAAAACCTCACATGCCACCGTCCGAGCACTGAACTCCTGGGGGACCGTCAGTC 753
          |||||||
```



VERSION	CR604961.1	GI:50485768
KEYWORDS	HTC; CNSLT_CDNA	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished	
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Paraday Avenue	
REFERENCE	2 (bases 1 to 1091)	
AUTHORS	Genoscope.	
TITLE	Direct Submission	
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
COMMENT	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	
FEATURES	Location/Qualifiers	
source	1..1091	
ORIGIN		
Query Match	49.6%; Score 682.4; DB 3; Length 1091;	
Best Local Similarity	99.9%; Pred. No. 1.4e-178;	
Matches	683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	694	GACAAAACCTCACATGCCCCCGTCCCGACACCTCACTGATCTCCCGGACCGTCAGTC 753
Db	323	GACAAAACCTCACATGCCCCCGTCCCGACACCTCACTGATCTCCCGGACCGTCAGTC 382
Qy	754	TTCTCTTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGACCGTCAGGTCTACA 813
Db	383	TTCTCTTTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGACCGTCAGGTCTACA 442
Qy	814	TGCGTGTGTGTGACGTGACCGACGACGACCTTGAGTCAAGTTCACTGGTACGTGAC 873
Db	443	TGCGTGTGTGTGACGTGACCGACGACGACCTTGAGTCAAGTTCACTGGTACGTGAC 502
Qy	874	GGCGTGTGTGATCAATATGCAAGACAAAGCCGCGGAGGACGATACAAACAGCAGTAC 933
Db	503	GGCGTGTGTGATCAATATGCAAGACAAAGCCGCGGAGGACGATACAAACAGCAGTAC 562
Qy	934	CGTGTGTGTGACGTCTCTACCGCTCTGCAACGAGACTGGCTGAATGGCAAGGATACAAG 993
Db	563	CGTGTGTGTGACGTCTCTACCGCTCTGCAACGAGACTGGCTGAATGGCAAGGATACAAG 622
Qy	994	TGCAGGTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAACCATCTTCCAAAGCCAAA 1053
Db	623	TGCAAGGTCTCCAAACAAAGCCCTCCAGCGCCCATCGAGAAACCATCTTCCAAAGCCAAA 682
Qy	1054	GGGAGCGCCCGAGAACACACAGGTGTACACCTGTCCCGCCCATCCCGGATGAGCTGACCAAG 1113
Db	683	GGGAGCGCCCGAGAACACACAGGTGTGTACACCTGTCCCGCCCATCCCGGATGAGCTGACCAAG 742
Qy	1114	AACAGGTCTAGCGCTGACCTGCTGTGTCAAAAGGCTTCTATCCCGAGGACATCGCCGTGGAG 1173
Db	743	AACAGGTCTAGCGCTGACCTGCTGTGTCAAAAGGCTTCTATCCCGAGGACATCGCCGTGGAG 802
Qy	1174	TGGGAGAGCAATGGGAGCGCGGAGAACAACTCAAGACCAACCGCTCCCGTGTGAGTCC 1233
Db	803	TGGGAGAGCAATGGGAGCGCGGAGAACAACTCAAGACCAACCGCTCCCGTGTGAGTCC 862



```
REFERENCE 2 (bases 1 to 1100)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES             Location/Qualifiers
     source          1..1100
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS01081YF02"
                     /tissue_type="Placenta Cot 25-normalized"
                     /plasmid="pCMVSPORT_6"
ORIGIN
Query Match      49.6%; Score 682.4; DB 3; Length 1100;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 694 GACAAACTCACACATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGACCGTCAGTC 753
Db 319 GACAAACTCACACATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGACCGTCAGTC 378
QY 754 TTCCTCTTCCCCCAGAACCCCAAGAGACCTTCATGATCTCCGAGACCCCTGAGTGTACA 813
Db 379 TTCCTCTTCCCCCAGAACCCCAAGAGACCTTCATGATCTCCGAGACCCCTGAGTGTACA 438
QY 814 TCGGTGGTGGTGGAGTGAGCCAGACACCGAGACCTTGAGTCAAGTCAACTGGTACGTGAC 873
Db 439 TCGGTGGTGGTGGAGTGAGCCAGACACCGAGACCTTGAGTCAAGTCAACTGGTACGTGAC 498
QY 874 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGTAC 933
Db 499 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGTAC 558
QY 934 CTGTGGTTCAGCGTCTCAACCGTCTTGACACAGGACTGCTGCTGAATGGCAAGGATACAG 993
Db 559 CGTGTGGTTCAGCGTCTCAACCGTCTTGACACAGGACTGCTGCTGAATGGCAAGGATACAG 618
QY 994 TGCAGGTCTCCAAACAAAGCCCTCCCGACCCCATCGAGAAACCATCTCCAAAGCCAAA 1053
Db 619 TGCAGGTCTCCAAACAAAGCCCTCCCGACCCCATCGAGAAACCATCTCCAAAGCCAAA 678
QY 1054 GGGCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAG 1113
Db 679 GGGCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAG 738
QY 1114 AACAGGTTCAGCTGACCTGCTGCTGCTCAAAGGCTTCTATTCAGCGACATGCGCTGGAG 1173
Db 739 AACAGGTTCAGCTGACCTGCTGCTGCTCAAAGGCTTCTATTCAGCGACATGCGCTGGAG 798
QY 1174 TGGGAGAGCAATGGGAGCGCGAGAACACTACAGACCAACCGCTCCCGTCTGCACTCC 1233
Db 799 TGGGAGAGCAATGGGAGCGCGAGAACAACTACAGACCAACCGCTCCCGTCTGCACTCC 858
QY 1234 GACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGAGGTGGCAGCAGGG 1293
Db 859 GACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGACAAGAGAGGTGGCAGCAGGG 918
QY 1294 AACGTCTTCTATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGAGAAGAGC 1353
Db 919 AACGTCTTCTATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGAGAAGAGC 978
QY 1354 CTCTCCCTGTCTCCGGGTAATGA 1377
Db 979 CTCTCCCTGTCTCCGGGTAATGA 1002
```

```
RESULT 13
CR601777
LOCUS full-length cDNA clone CS0CAP0081F07 of Thymus of Homo sapiens
DEFINITION (human).
ACCESSION CR601777 GI:50482584
VERSION CR601777.1
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
          1 (bases 1 to 1102)
          Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
          Full-length cDNA libraries and normalization
          Unpublished
          Contact : Feng Liang Email : fliang@lifetech.com URL :
          http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
          Faraday Avenue
          2 (bases 1 to 1102)
          Genoscope.
          Direct Submission
          Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
          BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
          - Web : www.genoscope.cns.fr)
          1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
          end enriched, double-strand cDNA was digested with Not I and cloned
          into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
          was normalized. Library was constructed by Life Technologies, a
          division of Invitrogen.
          Location/Qualifiers
          1..1102
          /organism="Homo sapiens"
          /mol_type="mRNA"
          /db_xref="taxon:9606"
          /clone="CS0CAP0081F07"
          /tissue_type="Thymus"
          /plasmid="pCMVSPORT_6"
ORIGIN
Query Match      49.6%; Score 682.4; DB 3; Length 1102;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 694 GACAAACTCACACATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGACCGTCAGTC 753
Db 319 GACAAACTCACACATGCCACCGTCCCGCAGCACCTGAACTCTCTGGGGGACCGTCAGTC 378
QY 754 TTCCTCTTCCCCCAGAACCCCAAGACACCTCATGATCTCCCGACCCCTTGAGTGTACA 813
Db 379 TTCCTCTTCCCCCAGAACCCCAAGACACCTCATGATCTCCCGACCCCTTGAGTGTACA 438
QY 814 TCGGTGGTGGTGGAGTGAGCCAGACACCTTGAGGTCAAAGTTCAACTGGTACGTGAC 873
Db 439 TCGGTGGTGGTGGAGTGAGCCAGACACCTTGAGGTCAAAGTTCAACTGGTACGTGAC 498
QY 874 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGTAC 933
Db 499 GCGGTGGAGGTGCATAATGCCAAGACAAAGCCGCGGAGGAGCAGTACAAACAGCACGTAC 558
QY 934 CTGTGGTTCAGCGTCTCAACCGTCTTGACACAGGACTGCTGCTGAATGGCAAGGATACAG 993
Db 559 CGTGTGGTTCAGCGTCTCAACCGTCTTGACACAGGACTGCTGCTGAATGGCAAGGATACAG 618
QY 994 TGCAGGTCTCCAAACAAAGCCCTCCCGACCCCATCGAGAAACCAATCTCCAAAGCCAAA 1053
Db 619 TGCAGGTCTCCAAACAAAGCCCTCCCGACCCCATCGAGAAACCAATCTCCAAAGCCAAA 678
QY 1054 GGGCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAG 1113
Db 679 GGGCAGCCCCGAGAACCAAGGTGTACACCTGCCCCCATCCCGGATGAGTGCACCAAG 738
```





/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="CS0DE010YH13"  
/tissue\_type="placenta"  
/plasmid="PCWSPORI\_6"

ORIGIN

```
Query Match          49.6%; Score 682.4; DB 3; Length 1103;
Best Local Similarity 99.9%; Pred. No. 1.4e-178;
Matches 683; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 694 GACAAACTCACACATGCCACCGTGGCCAGACCACTGAACTCTCTGGGGGACCCGTCAATC 753
Db 319 GACAAACTCACACATGCCACCGTGGCCAGACCACTGAACTCTCTGGGGGACCCGTCAATC 378
QY 754 TTCCTCTTCCCTCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 813
Db 379 TTCCTCTTCCCTCCCAAAACCCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCA 438
QY 814 TCGGTGGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 873
Db 439 TCGGTGGTGGTGGAGCTGAGCCACGAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAC 498
QY 874 GCGGTGGAGGTGCATAAATGCCAAAGCAAAAGCCGCGGAGGAGCAGTACAACAGCACGTAC 933
Db 499 GCGGTGGAGGTGCATAAATGCCAAAGCAAAAGCCGCGGAGGAGCAGTACAACAGCACGTAC 558
QY 934 CGTGTGGTCAGGTCCTTCACTGCTCTGACACGAGACTGGCTGAATGGCAAGGAGTACAAG 993
Db 559 CGTGTGGTCAGGTCCTTCACTGCTCTGACACGAGACTGGCTGAATGGCAAGGAGTACAAG 618
QY 994 TGCAAGGTCTCCAAACAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA 1053
Db 619 TGCAAGGTCTCCAAACAAGCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAA 678
QY 1054 GGGCAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAG 1113
Db 679 GGGCAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAG 738
QY 1114 AACCAAGGTCAAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATGCGCGTGGAG 1173
Db 739 AACCAAGGTCAAGCTGACCTGCTGCTCAAGGCTTCTATCCAGCGACATGCGCGTGGAG 798
QY 1174 TGGGAGAGCAATGGGCAGCCGAGAACCAACTACAAGACACAGCCCTCCCGTGTGGACTCC 1233
Db 799 TGGGAGAGCAATGGGCAGCCGAGAACCAACTACAAGACACAGCCCTCCCGTGTGGACTCC 858
QY 1234 GAGGCTCTTCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 1293
Db 859 GAGGCTCTTCTTCTTCTTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG 918
QY 1294 AAGTCTTCTCATGTGCTGATGATGAGGCTCTGCAACACCACTACACCGAGAGAGC 1353
Db 919 AAGTCTTCTCATGTGCTGATGATGAGGCTCTGCAACACCACTACACAGAGAGC 978
QY 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377
Db 979 CTCTCCCTGTCTCCGGGTAAATGA 1002
```

Search completed: August 27, 2005, 09:41:10  
Job time : 4871.12 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 23:31:34 ; Search time 248.401 Seconds  
(without alignments)  
9070.618 Million cell updates/sec

Title: US-10-009-852-15  
Perfect score: 1377  
Sequence: 1 atggtcagctactgggacac.....cctgtctccggtaaatga 1377

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1377	100.0	1377	4	US-09-773-877B-25
2	1328.4	96.5	1453	4	US-09-773-877B-21
3	1049.2	76.2	1444	4	US-09-773-877B-23
4	1039	75.5	1359	4	US-09-773-877B-15
5	1032.4	75.0	1389	4	US-09-773-877B-17
6	987.4	71.7	1674	4	US-09-773-877B-13
7	982.4	71.3	1704	4	US-09-773-877B-19
8	980.8	71.2	1704	4	US-09-773-877B-11
9	686	49.8	2043	3	US-08-227-496C-14
10	684	49.7	705	4	US-09-023-655-1223
11	684	49.7	1019	3	US-09-178-869-1
12	684	49.7	1019	4	US-09-761-413-1
13	684	49.7	1182	3	US-09-180-100-18
14	684	49.7	1428	1	US-08-488-376-19
15	684	49.7	1428	2	US-08-634-223-19
16	684	49.7	1428	2	US-08-634-224-19
17	684	49.7	1428	2	US-08-634-400-19
18	684	49.7	1428	2	US-08-635-878-19
19	684	49.7	1428	2	US-08-770-057-19
20	684	49.7	1428	3	US-09-335-697B-19
21	684	49.7	1428	3	US-09-335-697B-19
22	684	49.7	1428	4	US-09-740-002-19
23	684	49.7	1431	3	US-08-487-550-3
24	684	49.7	1431	3	US-08-487-550-11
25	684	49.7	1431	4	US-09-526-098-3
26	684	49.7	1431	4	US-09-526-098-11
27	684	49.7	1431	4	US-09-383-916-3

28	684	49.7	1431	4	US-09-383-916-11	Sequence 11, Appl
29	684	49.7	1437	3	US-08-487-550-7	Sequence 7, Appl
30	684	49.7	1437	4	US-09-526-098-7	Sequence 7, Appl
31	684	49.7	1437	4	US-09-383-916-7	Sequence 7, Appl
32	684	49.7	1458	4	US-08-030-175-6	Sequence 6, Appl
33	684	49.7	1458	4	US-08-030-175-7	Sequence 7, Appl
34	684	49.7	1467	4	US-08-030-175-5	Sequence 5, Appl
35	684	49.7	1494	4	US-09-499-846-5	Sequence 5, Appl
36	684	49.7	1578	4	US-09-499-846-3	Sequence 3, Appl
37	684	49.7	1599	4	US-09-023-655-1120	Sequence 1120, Ap
38	684	49.7	1617	2	US-08-378-939-9	Sequence 9, Appl
39	684	49.7	1720	4	US-09-746-359A-52	Sequence 52, Appl
40	684	49.7	1869	4	US-09-499-846-1	Sequence 1, Appl
41	684	49.7	3477	4	US-09-313-942-25	Sequence 25, Appl
42	684	49.7	3507	4	US-09-313-942-23	Sequence 23, Appl
43	684	49.7	9209	1	US-08-149-099C-3	Sequence 3, Appl
44	684	49.7	9209	1	US-08-476-275-2	Sequence 2, Appl
45	684	49.7	9209	2	US-08-478-967A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1  
US-09-773-877B-25  
; Sequence 25, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.0  
; SEQ ID NO 25  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VEGFR1R2.FcdeltaCl(a) Receptor  
; NAME/KEY: CDS  
; LOCATION: (1)..(1377)  
US-09-773-877B-25

Query Match		100.0%;	Score 1377;	DB 4;	Length 1377;
Best Local Similarity		100.0%;	Pred. No. 0;		
Matches 1377;		Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
Qy	1	ATGCTCAGCTACTCGGACACCGGGGTCTGCTGTGCGCGTGTCTCAGCTGTCTGCTCTC	60		
Db	1	ATGCTCAGCTACTCGGACACCGGGGTCTGCTGTGCGCGTGTCTCAGCTGTCTGCTCTC	60		
Qy	61	ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGACAGTGAATC	120		
Db	61	ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGACAGTGAATC	120		
Qy	121	CCCGAAATTATACATGACTGAAGGAGGAGCTCGTCATTCCTCGCGGGTTACGTCA	180		
Db	121	CCCGAAATTATACATGACTGAAGGAGGAGCTCGTCATTCCTCGCGGGTTACGTCA	180		
Qy	181	CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTCGACCTTTTGATCCCTGATGGAANA	240		
Db	181	CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTCGACCTTTTGATCCCTGATGGAANA	240		
Qy	241	CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATA	300		
Db	241	CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAAGTACAAAGAAATA	300		
Qy	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAATCTCTACA	360		
Db	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAATCTCTACA	360		

Qy	361	CATCGACAAACCAATACAAATCATATAGATGTGGTTCTTGAGTCCGCTCTCATGGAAATTGAAC	420
Db	361	CATCGACAAACCAATACAAATCATATAGATGTGGTTCTTGAGTCCGCTCTCATGGAAATTGAAC	420
Qy	421	TCTGTGTGGAGAAAAGCTTTGCTTAAATTTGTATACACAAGAACTGAACATAAATGTGGGAT	480
Db	421	TCTGTGTGGAGAAAAGCTTTGCTTAAATTTGTATACACAAGAACTGAACATAAATGTGGGAT	480
Qy	481	GACTTCAACTGGGAATACCCCTTCTTGAAGCATCAGCATAGAAACCTTGTAAACCCGAGAC	540
Db	481	GACTTCAACTGGGAATACCCCTTCTTGAAGCATCAGCATAGAAACCTTGTAAACCCGAGAC	540
Qy	541	CTAAAAACCCAGTCTGGAGTGAGATGAAGAAAATTTTGTAGACACTTAACTATAGATGGT	600
Db	541	CTAAAAACCCAGTCTGGAGTGAGATGAAGAAAATTTTGTAGACACTTAACTATAGATGGT	600
Qy	601	GTAACCCGGAGTGACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGGTGATCACCAG	660
Db	601	GTAACCCGGAGTGACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGGTGATCACCAG	660
Qy	661	AAGAACAGCAATTTGTGAGGGTCCATGAAAAGGACAAAACCTCACATGCCCCACCGTGC	720
Db	661	AAGAACAGCAATTTGTGAGGGTCCATGAAAAGGACAAAACCTCACATGCCCCACCGTGC	720
Qy	721	CCAGCACTGNACTCTGGGGGGACCGTCAGTCTTCTTCCCTCCCAAAACCCAGGAC	780
Db	721	CCAGCACTGNACTCTGGGGGGACCGTCAGTCTTCTTCCCTCCCAAAACCCAGGAC	780
Qy	781	ACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGAGCTGAGGCACGAA	840
Db	781	ACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGAGCTGAGGCACGAA	840
Qy	841	GACCTGAGGTCAAAGTTCAACTGTGAACGCGGTGGAGGTGCAATAATGCCAAGACA	900
Db	841	GACCTGAGGTCAAAGTTCAACTGTGAACGCGGTGGAGGTGCAATAATGCCAAGACA	900
Qy	901	AAGCCGGGGAGGACGATCAACAGCAGCATACCGTGTGGTCAGGTCCTCACCGTCTTG	960
Db	901	AAGCCGGGGAGGACGATCAACAGCAGCATACCGTGTGGTCAGGTCCTCACCGTCTTG	960
Qy	961	CACCAGGACTGGCTGAATGGCAAGGATACAAGTGCAAGTCTCCACAAGCCCTCCCA	1020
Db	961	CACCAGGACTGGCTGAATGGCAAGGATACAAGTGCAAGTCTCCACAAGCCCTCCCA	1020
Qy	1021	GCCCCCATCGAGAAAAACATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTAC	1080
Db	1021	GCCCCCATCGAGAAAAACATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCAAGGTGTAC	1080
Qy	1081	ACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTGACCTGACCTGCTGCTC	1140
Db	1081	ACCTGCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTGACCTGACCTGCTGCTC	1140
Qy	1141	AAAGGCTTCTATCCACGCGACATCCCGTGGAGTGGGAGCAATGGCAGCCGAGAAC	1200
Db	1141	AAAGGCTTCTATCCACGCGACATCCCGTGGAGTGGGAGCAATGGCAGCCGAGAAC	1200
Qy	1201	AACCTAAGACCAAGCTCCCGTGGTGGATCCGACGGCTCTTCTTCTCTACAGCAAG	1260
Db	1201	AACCTAAGACCAAGCTCCCGTGGTGGATCCGACGGCTCTTCTTCTCTACAGCAAG	1260
Qy	1261	CTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTTCTTCTCATGCTCCGTATGCAT	1320
Db	1261	CTACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAACGTTCTTCTCATGCTCCGTATGCAT	1320
Qy	1321	GAGGCTCTGCAACACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1377
Db	1321	GAGGCTCTGCAACACCACTACACGACAGAGCCCTCTCCCTGTCTCCGGGTAAATGA	1377

```

1  / GENERAL INFORMATION:
2  / APPLICANT: Xia, Yu-Ping et al.
3  / TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
4  / FILE REFERENCE: REG 710b
5  / CURRENT APPLICATION NUMBER: US/09/773,877B
6  / CURRENT FILING DATE: 2001-01-31
7  / NUMBER OF SEQ ID NOS: 27
8  / SOFTWARE: PatentIn version 3.0
9  / SEQ ID NO 21
10 / LENGTH: 1453
11 / TYPE: DNA
12 / ORGANISM: Artificial Sequence
13 / FEATURE:
14 / NAME/KEY: CDS
15 / LOCATION: (69) .. (1442)
16 / US-09-773-877B-21
17 /
18 / OTHER INFORMATION: FtlD2.FlkID3.FcdeltaC1(a)Receptor
19 /
20 /
21 /
22 /
23 /
24 /
25 /
26 /
27 /
28 /
29 /
30 /
31 /
32 /
33 /
34 /
35 /
36 /
37 /
38 /
39 /
40 /
41 /
42 /
43 /
44 /
45 /
46 /
47 /
48 /
49 /
50 /
51 /
52 /
53 /
54 /
55 /
56 /
57 /
58 /
59 /
60 /
61 /
62 /
63 /
64 /
65 /
66 /
67 /
68 /
69 /
70 /
71 /
72 /
73 /
74 /
75 /
76 /
77 /
78 /
79 /
80 /
81 /
82 /
83 /
84 /
85 /
86 /
87 /
88 /
89 /
90 /
91 /
92 /
93 /
94 /
95 /
96 /
97 /
98 /
99 /
100 /

```

Query Match	96.5%	Score 1328.4	DB 4	Length 1453
Best Local Similarity	98.6%	Pred. No. 0		
Matches 1367	Conservative	0	Mismatches 1	Indels 18
				Gaps 2
Qy	1	ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGGCGCGTGTCTCAGCTGCTGCTGCTCTC	60	
Db	69	ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGGCGCGTGTCTCAGCTGCTGCTGCTCTC	128	
Qy	61	ACAGGATCTAGTTCCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC	120	
Db	129	ACAGGATCTAGTTCCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC	179	
Qy	121	CCCGAATTAATACATGACTGAAGGAAGGAGCTGCTCATTTCCCTGCCGGGTACGTCA	180	
Db	180	CCCGAATTAATACATGACTGAAGGAAGGAGCTGCTCATTTCCCTGCCGGGTACGTCA	239	
Qy	181	CCTAAACATCACTGTTACTTTTAAAAAGTTTCCACTTTGACACTTTGATCCCTGATGAAAA	240	
Db	240	CCTAAACATCACTGTTACTTTTAAAAAGTTTCCACTTTGACACTTTGATCCCTGATGAAAA	299	
Qy	241	CGCATAAATCTGGGACAGTAGAAAAGGCTTCATCATATCAAAATGCAACGTAACAAGAAATA	300	
Db	300	CGCATAAATCTGGGACAGTAGAAAAGGCTTCATCATATCAAAATGCAACGTAACAAGAAATA	359	
Qy	301	GGGGTCTGACCTGTGAGCAACAGTCAATGGGCAATTTGTAAGCAAAACTATCTCACA	360	
Db	360	GGGGTCTGACCTGTGAGCAACAGTCAATGGGCAATTTGTAAGCAAAACTATCTCACA	419	
Qy	361	CATCGAACAACCAATCAATCATAGATGTGGTTCTCGAGTCCGTCTCATGAAATTGAACATA	420	
Db	420	CATCGAACAACCAATCAATCATAGATGTGGTTCTCGAGTCCGTCTCATGAAATTGAACATA	479	
Qy	421	TCTGTTGGAGAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT	480	
Db	480	TCTGTTGGAGAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGGATT	539	
Qy	481	GACTTCAACTGGGAATACCCCTCTTCGAAGCATCAGCATGAAGAACTGTGTAACCCGAGAC	540	
Db	540	GACTTCAACTGGGAATACCCCTCTTCGAAGCATCAGCATGAAGAACTGTGTAACCCGAGAC	599	
Qy	541	CTAAAAACCCAGTCTGGGAGTGAAGTGAAGAAATTTTTCGACACCTTTAACTATAGATGGT	600	
Db	600	CTAAAAACCCAGTCTGGGAGTGAAGTGAAGAAATTTTTCGACACCTTTAACTATAGATGGT	659	
Qy	601	GTAAACCGGAGTGACCAAGATTGTACA CTTGTGTCAGCATCCAGTGGGCTGATGACCAAG	660	
Db	660	GTAAACCGGAGTGACCAAGATTGTACA CTTGTGTCAGCATCCAGTGGGCTGATGACCAAG	719	
Qy	661	AAGAAACAGCACATTTGTTCAGGGTCCATGAAAAAG-----GACAAAACTCACACATGC	711	
Db	720	AAGAAACAGCACATTTGTTCAGGGTCCATGAAAAAGGGCCCGGGGACAAAACTCACACATGC	779	
Qy	712	CCACCGTGCCACGACCTGAACTCCTGGGGGACCGGTCACTCTTCCTCTTCCCCCCAAAA	771	
Db	780	CCACCGTGCCACGACCTGAACTCCTGGGGGACCGGTCACTCTTCCTCTTCCCCCCAAAA	839	

Qy	772	CCCAAGGACACCTCATGATCTCCGGAGCCCTCAGGTCACATCGCTGGTGGTGGACGTG	831
Db	840	CCCAAGGACACCTCATGATCTCCGGAGCCCTCAGGTCACATCGCTGGTGGTGGACGTG	899
Qy	832	AGCCACGAAGACCTTGAGGTCAGATTCAACTGGTACGTGGACGCGCTGGAGGTGCATAAT	891
Db	900	AGCCACGAGACCTTGAGGTCAGATTCAACTGGTACGTGGACGCGCTGGAGGTGCATAAT	959
Qy	892	GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAACCTGTGGTCAGCGTCTCTC	951
Db	960	GCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTAACCTGTGGTCAGCGTCTCTC	1019
Qy	952	ACCGTCTCTGCACACGAGCTGCTCAATGGCAAGGAGTACAAGTGCAGAGGTCTCCAAACAA	1011
Db	1020	ACCGTCTCTGCACACGAGCTGCTCAATGGCAAGGAGTACAAGTGCAGAGGTCTCCAAACAA	1079
Qy	1012	GCCCTCCAGCCGCCCATCGAGAAACCATCTTCAAAGCCAAAGGGCAGCCCCGAGAACCA	1071
Db	1080	GCCCTCCAGCCGCCCATCGAGAAACCATCTTCAAAGCCAAAGGGCAGCCCCGAGAACCA	1139
Qy	1072	CAGGTGTACACCTTGCCCCCATCCCGGGAATGAGCTGACCAAGAACGAGGTGAGGCTGACC	1131
Db	1140	CAGGTGTACACCTTGCCCCCATCCCGGGAATGAGCTGACCAAGAACGAGGTGAGGCTGACC	1199
Qy	1132	TGCCTGGTCAAAGGCTTCTATCCCAACGACACATCCCGGTGGAGTCGGAGAGCAATGGGCAG	1191
Db	1200	TGCCTGGTCAAAGGCTTCTATCCCAACGACACATCCCGGTGGAGTCGGAGAGCAATGGGCAG	1259
Qy	1192	CCGGAGAACCACTACAAGACCAACGCCCTCCCGTGTGGACTCCGACGGCTCTCTTCTCTCTC	1251
Db	1260	CCGGAGAACCACTACAAGACCAACGCCCTCCCGTGTGGACTCCGACGGCTCTCTTCTCTCTC	1319
Qy	1252	TACAGCAAGCTCACCGTGGACAAGACGAGGTGGCAGCAGGGGAAAGCTTCTCATGTCTCC	1311
Db	1320	TATAGCAAGCTCACCGTGGACAAGACGAGGTGGCAGCAGGGGAAAGCTTCTCATGTCTCC	1379
Qy	1312	GTGATGATGAGGCTCTGCACAAACCACTACACGACGAGAAGCCCTCTCCCTGTCTCCGGGT	1371
Db	1380	GTGATGATGAGGCTCTGCACAAACCACTACACGACGAGAAGCCCTCTCCCTGTCTCCGGGT	1439
Qy	1372	AAATGA	1377
Db	1440	AAATGA	1445

### RESULT 3

US-09-773-877B-23

00 03 713 0772 23  
; Sequence 23, Application US/09773877B

; Patent No. 6833349

GENERAL INFORMATION:

APPLICANT: Xia, Yu-Ping

; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

; FILE REFERENCE: REG 710b

; CURRENT APPLICATION NUMBER: US/09/773,877B

; CURRENT FILING DATE: 2001-01-31

; NUMBER OF SEQ ID NOS: 27

```
; SOFTWARE: PatentIn version 3.0
```

; SEQ ID NO 23

; LENGTH: 1444

TYPE: DNA

ORGANISM: Artificial Sequence

```

;
; FEATURE:
;
; OTHER INFORMATION: F1+D2 VECPRD3 ECDEL+AC1 (a) Recent or

```

```

; OTHER INFORMATION: FT1D2.VEGFR3D3.Fcdelta1(a)Receptor
: NAME/KEY: CDS

```

```

; NAME/KEY: CDS
; LOCATION: (69) (1436)

```

US-09-773-877B-23

C7-B/18-C/1-EN

Query Match	76.2%	Score 1049.2	DB 4	Lenath 1444
-------------	-------	--------------	------	-------------

Query Match 78.2%; Score 1049.2; DB 4; Length 1444;  
Best Local Similarity 86.7%; Pred. No. 6.7e-271;

Best local similarity 86.74; Fied: NO: 8.7e-271;  
Matches 1201: Conservative 0: Mismatches 158: Indels 27: Gaps 3:

matchers 1201; conservative 0; mismatches 130; index 27; gaps

[illegible]



Db 1131 CAGGTGTACACCTGTCGCCCCATCCGGGATGAGCTGACCAAGAACCCAGGTGAGCTGACC 1190  
Qy 1132 TGCCCTGGTCAAGGGCTTCTATCCAGCGACATGCGCGTGGAGTGGAGCAATGGGGCAG 1191  
Db 1191 TGCCCTGGTCAAGGGCTTCTATCCAGCGACATGCGCGTGGAGTGGAGCAATGGGGCAG 1250  
Qy 1192 CCGGAGAACAACTACAAGACCAAGCCCTCCGCTGCTGGACTCGGAGCGCTCTTCTCTC 1251  
Db 1251 CCGGAGAACAACTACAAGACCAAGCCCTCCGCTGCTGGACTCGGAGCGCTCTTCTCTC 1310  
Qy 1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCC 1311  
Db 1311 TATAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGGAAAGCTTCTCATGCTCC 1370  
Qy 1312 GTGATGATGAGGCTCTGCAACAACCACTACAGCGAGAAAGAGCGCTCTCTGCTCCGGGT 1371  
Db 1371 GTGATGATGAGGCTCTGCAACAACCACTACAGCGAGAAAGAGCGCTCTCTGCTCCGGGT 1430  
Qy 1372 AAATGA 1377  
Db 1431 AAATGA 1436

## RESULT 4

US-09-773-877B-15

; Sequence 15, Application US/09773877B

; Patent No. 6833349

; GENERAL INFORMATION:

; APPLICANT: Xia, Yu-Ping et al.

; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES

; FILE REFERENCE: REG 710b

; CURRENT APPLICATION NUMBER: US/09/773,877B

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 15

; LENGTH: 1359

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Fc1(2-3 deltaB) -Fc (Mut2)

; NAME/KEY: CDS

; LOCATION: (1)...(1359)

US-09-773-877B-15

Query Match 75.5%; Score 1039; DB 4; Length 1359;  
Best Local Similarity 86.3%; Pred. No. 3.5e-268;  
Matches 1189; Conservative 0; Mismatches 170; Indels 18; Gaps 3;

Qy 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGGTGCTCAGCTGTCTGCTCTC 60  
Db 1 ATGGTCAGCTACTGGGACACCGGGTCTGCTGTGGCGGTGCTCAGCTGTCTGCTCTC 60  
Qy 61 ACAGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGATCTAGTTCGGGA-----GGTAGACCTTTCGTAGAGATGTACAGTGAATC 111  
Qy 121 CCCGAAATTAACATGACTGAAGGAGGAGCTGCTCATTCCTCGCGGGTTACGTCA 180  
Db 112 CCCGAAATTAACATGACTGAAGGAGGAGCTGCTCATTCCTCGCGGGTTACGTCA 171  
Qy 181 CCTAACATCATGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAA 240  
Db 172 CCTAACATCATGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAA 231  
Qy 241 CGCATAACTCTGGGACAGTAGAAGGGCTTCAATATCAAAATGCAAGTACAAAGAAATA 300  
Db 232 CGCATAACTCTGGGACAGTAGAAGGGCTTCAATATCAAAATGCAAGTACAAAGAAATA 291  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATCGGCAATTTGTATAAGACAAACTATCTACA 360  
Db 292 GGGCTTCTGACCTGTGAAGCAACAGTCAATCGGCAATTTGTATAAGACAAACTATCTACA 351

## RESULT 5

US-09-773-877B-17

; Sequence 17, Application US/09773877B

; Patent No. 6833349

Qy 361 CATCGACAAACCAATACAACTAGATGTGGTCTGAGTCCGTCTCATGGAATGAACCTA 420  
Db 352 CATCGACAAACCAATACAACTAGATGTCAAATAAGCACACCCGCCAGTCAAAATTA 411  
Qy 421 TCTGTTGCGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAATCTAAATGTGGGAT 480  
Db 412 CTTAGAGGCCATCTCTTGTCTCAATGTACTGCTACCACTCCCTTTGAACACAGAGTT 471  
Qy 481 GACTTCAACTGGGAATACCCCTTCTTGAAGCATCAGCATAAAGAACTTTGTAACCGAGAC 540  
Db 472 CAATGACCTGGAGTTACCTCTGATGAATTTGACAAAGCAATTCCTCATGCAACATATTC 531  
Qy 541 CTAAAAACCCAGTCTGGAGTGAGATGAAGAAATTTTGGACACCTTAACTATAGATGGT 600  
Db 532 TACAGTGTCTTACTATTGTACAAATGCAAGAAATGCAAGAAAGCAAAAGGACTTTTACTTTCGT 591  
Qy 601 GTAAACCCGAGTACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Db 592 GTAA--GGAGTGGACCATCAATCAATCTGTTAAACCTC-----AGTGCATATATAT 642  
Qy 661 AAGAACAGCACATTTGTCAAGGTCCATGAAAGAGCAAAACTCAACATGCCCCACCGTGC 720  
Db 643 GATAAAGCAGGCCCGGGCGAGCCCAATCTTGTGACAAAACTCACACATGCCACCGTGC 702  
Qy 721 CCAGCACCCTGAACTCTCCCGGACCCCTGAGGTCACTGCGTGGTGGTGGAGCGTGAAGCA 840  
Db 703 CCAGCACCCTGAACTCTCCCGGAGCCCGTCACTCTTCTCTTCCCGCCCAAAACCCAGGAC 762  
Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCACTGCGTGGTGGTGGAGCGTGAAGCAAGAA 840  
Db 763 ACCCTCATGATCTCCCGGACCCCTGAGGTCACTGCGTGGTGGTGGAGCGTGAAGCAAGAA 822  
Qy 841 GACCTGAGTCAAGTTCAACTGGTACGTGGAAGCGGTGAGGTGCAATAATGCAAGACA 900  
Db 823 GACCTGAGTCAAGTTCAACTGGTACGTGGAAGCGGTGAGGTGCAATAATGCAAGACA 882  
Qy 901 AAGCGCGGAGGAGGAGTACAAAGCAAGGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCCA 1020  
Db 883 AAGCGCGGAGGAGGAGTACAAAGCAAGGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCCA 942  
Qy 961 CACCAGGACTGGCTGAATGCAAGGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCCA 1020  
Db 943 CACCAGGACTGGCTGAATGCAAGGAGTACAAGTGAAGGTCTCCAAACAAAGCCCTCCCA 1002  
Qy 1021 GCCCCATCGAGAAACCACTCTCCAAAGCAAGGGCAGCCCGAGAAACCAAGGTGTAC 1080  
Db 1003 GCCCCATCGAGAAACCACTCTCCAAAGCAAGGGCAGCCCGAGAAACCAAGGTGTAC 1062  
Qy 1081 ACCCTGCCCATCCCGGAGTGAACCAAGAACCAAGGTGAGCTGAGCTGCTGCTGCTGCTC 1140  
Db 1063 ACCCTGCCCATCCCGGAGTGAACCAAGAACCAAGGTGAGCTGAGCTGCTGCTGCTGCTC 1122  
Qy 1141 AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGACCGCGGAAC 1200  
Db 1123 AAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGAGAGCAATGGGACCGCGGAAC 1182  
Qy 1201 AACTAAGAACACCGCTCCCGTGTGGAATCCGAGCGGCTCTTCTTCTCTACAGCAAG 1260  
Db 1183 AACTAAGAACACCGCTCCCGTGTGGAATCCGAGCGGCTCTTCTTCTCTACAGCAAG 1242  
Qy 1261 CTCAACCGTGACAAAGAGCAGGTGGCAGAGGGGAACGTCTTCTCATGCTCCGCTGATGCAT 1320  
Db 1243 CTCAACCGTGACAAAGAGCAGGTGGCAGAGGGGAACGTCTTCTCATGCTCCGCTGATGCAT 1302  
Qy 1321 GAGGCTCTGCACAAACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1377  
Db 1303 GAGGCTCTGCACAAACCACTACAGCAGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1359

```
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(2-3)-Fc (Mut3)
; NAME/KEY: CDS
; LOCATION: (1)..(1389)
US-09-773-877B-17

Query Match      75.0%; Score 1032.4; DB 4; Length 1389;
Best Local Similarity 85.5%; Pred. No. 2.1e-266;
Matches 1201; Conservative 0; Mismatches 161; Indels 42; Gaps 3;

QY      1 ATGGTCAGCTACTGGGACACCGGGGCTCTGCTGCGCGCTGCTCAGCTGTGCTTCTC 60
DB      1 ATGGTCAGCTACTGGGACACCGGGGCTCTGCTGCGCGCTGCTCAGCTGTGCTTCTC 60

QY      61 ACAGGATCTAGTTCGCGAAGTGATACCGGTGAGACCTTTTCGTAGAGATGTACAGTGAATC 120
DB      61 ACAGGATCTAGTTCGCGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC 111

QY      121 CCGGAAATATATACATGACTGAAGAGAGGAGCTGCTCATTCCTCGCGGGTTACGTCA 180
DB      121 CCGGAAATATATACATGACTGAAGAGAGGAGCTGCTCATTCCTCGCGGGTTACGTCA 171

QY      181 CCTAACATCAGTGTACTTTTAAAGTTTCCATTGTGACCTTTGATCCCTGATGGAAA 240
DB      172 CCTAACATCAGTGTACTTTTAAAGTTTCCATTGTGACCTTTGATCCCTGATGGAAA 231

QY      241 CGCATAATCTGGGACAGTAGAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 300
DB      232 CGCATAATCTGGGACAGTAGAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 291

QY      301 GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTACA 360
DB      292 GGGCTTCTGACTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTACA 351

QY      361 CATCGACAAACCATACATCATAGATGTGTTCTGAGTCCGTCTCATGGAATGAACATA 420
DB      352 CATCGACAAACCATACATCATAGATGTCCAAATAAGCACACCAACGCCCAAGTCAAAATTA 411

QY      421 TCTGTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACATAAATGTGGGATT 480
DB      412 CTTAGAGGCCATACTCTTGTCTCAATTTGTACTGTCTACCATCTCCCTTGAACACAGAGTT 471

QY      481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCAATAAGAACTTTGTAACCGAGAC 540
DB      472 CAATATGACCTGGAGTTACCTT-----GATGAAAAAATAAGAGAGCTTCGTAAGGCA 525

QY      541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAATATATAGATGGT 600
DB      526 CGAATTGACCAAGCAATTTCCCATGCCAAATATTTCTACAGTGTCTTACTATTGACAAA 585

QY      601 GTAACCGGAGTGACCAAGGATTTGACACCTGTGCGAGCATCCAGTGGGCTGATGCCAAG 660
DB      586 ATGCAGAAACAAAGCAAGAGACTTTATCTTGTTCGTGAAGAGTGGACCATCATTTCAA 645

QY      661 AAGAACAGCAGCATTTGTCCAGGGTCCATGAAA-----G 693
DB      646 TCTGTAAACACCTCAGTCATATATATATGATAAGCAGCGCCCGGGGAGCCCAATCTGT 705

QY      694 GACAAACTCAGATGCCCAACCGTGCCAGCAGCTGAACTCTCTGGGGGAGCCGTCAGTC 753
DB      706 GACAAACTCAGATGCCCAACCGTGCCAGCAGCTGAACTCTCTGGGGGAGCCGTCAGTC 765

754 TTCCTCTTCCCTCCCAAAACCCAGGACACCTCTCATGATCTCCCGACCCCTGAGGTCA 813
766 TTCTCTTCTCCCTCCCAAAACCCAGGACACCTCTCATGATCTCCCGACCCCTGAGGTCA 825
814 TGCCTGGTGGTGGACGTCGAGCCACGAAGACCTCTGAGGTCAAGTTCAACTGTGACGTG 873
826 TGCCTGGTGGTGGACGTCGAGCCACGAAGACCTCTGAGGTCAAGTTCAACTGTGACGTG 885
874 GGCCTGGAGGTGCATATAATCCCAAGACCGCGGAGGAGCAGTACAACAGACGATAC 933
886 GGCCTGGAGGTGCATATAATCCCAAGACCGCGGAGGAGCAGTACAACAGACGATAC 945
934 CGTGTGGTTCAGCTCTCCTCAGCCGCTCTGTCACAGGACTGGCTGCAATGGCAAGAGTACA 993
946 CGTGTGGTTCAGCTCTCCTCAGCCGCTCTGTCACAGGACTGGCTGCAATGGCAAGAGTACA 1005
994 TGCAGGTCTCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCC 1053
1006 TGCAGGTCTCCAAACAAAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCCCTCCAGCC 1065
1054 GGGCAGCCCGGAGAACACAGGTGTACACCTGCGCCCTCCAGCCCTCCAGCCCTCCAGCC 1113
1066 GGGCAGCCCGGAGAACACAGGTGTACACCTGCGCCCTCCAGCCCTCCAGCCCTCCAGCC 1125
1114 AACAGGTTCAGCTCTGCTCTGCTCAAAAGCTTCTATCCAGCGCATCCCGGTGGAG 1173
1126 AACAGGTTCAGCTCTGCTCTGCTCAAAAGCTTCTATCCAGCGCATCCCGGTGGAG 1185
1174 TGGAGAGCAATGGGAGCGGAGAAACAACTACAGACCCAGCTCCCGTCTGAGCTCC 1233
1186 TGGAGAGCAATGGGAGCGGAGAAACAACTACAGACCCAGCTCCCGTCTGAGCTCC 1245
1234 GACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGAGCAGAGCAGGTCGACGAGGG 1293
1246 GACGGCTCTCTTCTCTCTACAGCAAGCTCACCGTGAGCAGAGCAGGTCGACGAGGG 1305
1294 AACGTCTTCTCATGCTCCGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1353
1306 AACGTCTTCTCATGCTCCGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1365
1354 CTCTCCCTGCTCCGGGTAAATGA 1377
1366 CTCTCCCTGCTCCGGGTAAATGA 1389

RESULT 6
US-09-773-877B-13
; Sequence 13, Application US/09773877B
; Patent No. 6833349
; GENERAL INFORMATION:
; APPLICANT: Xia, Yu-Ping et al.
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES
; FILE REFERENCE: REG 710b
; CURRENT APPLICATION NUMBER: US/09/773,877B
; CURRENT FILING DATE: 2001-01-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 1674
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flt1(1-3 deltaB) (Mut 1)
; NAME/KEY: CDS
; LOCATION: (1)..(1674)
US-09-773-877B-13

Query Match      71.7%; Score 987.4; DB 4; Length 1674;
Best Local Similarity 86.1%; Pred. No. 2.6e-254;
Matches 1119; Conservative 0; Mismatches 171; Indels 9; Gaps 2;

QY      79 AGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATATCCCGGAAATATATACATG 138
```

||||| 385 AGTGATACAGGTAGACCTTTCTGTAGATGTACAGTGAAATCCCGAAATATACATG 444  
Qy 139 ACTGAAGGAAGGAGCTCGTCAITCCCTGCCGGGTAGCTCACCTAAACATCACTGTTACT 198  
Db 445 ACTGAAGGAAGGAGCTCGTCAITCCCTGCCGGGTAGCTCACCTAAACATCACTGTTACT 504  
Qy 199 TTAAGAAAGTTTCACATTGACACTTTGATCCCTGATGGAACCAATCTGGGACAGT 258  
Db 505 TTAAGAAAGTTTCACATTGACACTTTGATCCCTGATGGAACCAATCTGGGACAGT 564  
Qy 259 AGAAGGCTTCATCATATCAATCAAAATGCAACGTACAAAGAAATAGGCTCTGACCTGTGAA 318  
Db 565 AGAAGGCTTCATCATATCAATCAAAATGCAACGTACAAAGAAATAGGCTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCACATCGACAAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCACATCGACAAACCAATACA 684  
Qy 379 ATCATAGATGGTTCGAGTCCGTCTCATGGAATTTGAATCTATCTGTTGGGAAAGCTT 438  
Db 685 ATCATAGATGGTTCGAGTCCGTCTCATGGAATTTGAATCTATCTGTTGGGAAAGCTT 744  
Qy 439 GTCTTAAATTTACAGCAAGAACTGAATCTGAGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTTAAATTTACAGCAAGAACTGAATCTGAGGATTTGACTTCAACTGGGAATAC 804  
Qy 499 CCTTCTTGAAGCATCAGCATAAGAACTTTGAAACCGAGACCTTAAACCCAGTCTGGG 558  
Db 805 CCTGATGAATTTGACCAAGCAATTTCCATGCCAATATTTCTACAGTGTCTTACTATT 864  
Qy 559 AGTGAGATGAAGAAATTTTGGAGCACTTAACTATAGATGGTGTAAACCGGAGTGACAA 618  
Db 865 GACAAATGCAAGAAACCAAGCAAAAGGACTTTATCTTGTCTGTAA---GGAGTGGACCA 921  
Qy 619 GGATTTGATACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAAGACAGACATTTGTC 678  
Db 922 TCATTCAATCTGTTAAACCTC-----AGTGATATATATGATAAGACGGCCCGGC 975  
Qy 679 AGGTTCCATGAAAGGACAAACTCACATATGCCACCGTCCGACGACCTGAACTCCTG 738  
Db 976 GAGCCCAATCTTGTGCAAAACTCACATATGCCACCGTCCGACGACCTGAACTCCTG 1035  
Qy 739 GGGGACCGTCAGTCTTCTCTCCGCCCAAAACCAAGGACACCTCATGATCTCCGG 798  
Db 1036 GGGGACCGTCAGTCTTCTCTCCGCCCAAAACCAAGGACACCTCATGATCTCCGG 1095  
Qy 799 ACCCTGAGGTACATGCGTGGTGGAGCGTGGAGCCAGCAAGACCTTGAGTCAAGTTC 858  
Db 1096 ACCCTGAGGTACATGCGTGGTGGAGCGTGGAGCCAGCAAGACCTTGAGTCAAGTTC 1155  
Qy 859 AACTGGTACGTGGACGGCGTGGAGGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAG 918  
Db 1156 AACTGGTACGTGGACGGCGTGGAGGTGCATATGCCAAGACAAAGCCGCGGAGGAGCAG 1215  
Qy 919 TACAACAGCATACCGTGGTGGAGGTGCATGCTTCAAGTCTGACAGGACTGCTGAAT 978  
Db 1216 TACAACAGCATACCGTGGTGGAGGTGCATGCTTCAAGTCTGACAGGACTGCTGAAT 1275  
Qy 979 GGCAGAGGTACAAGTGAAGTCTTCAAAAGGCTTCCAGGCCCCCATCGAGAAACC 1038  
Db 1276 GGCAGAGGTACAAGTGAAGTCTTCAAAAGGCTTCCAGGCCCCCATCGAGAAACC 1335  
Qy 1039 ATCTCCAAAGCCAAAGGCGACCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCGG 1098  
Db 1336 ATCTCCAAAGCCAAAGGCGACCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCGG 1395  
Qy 1099 GATGAGTGAACCAAGAACCGAGTCAAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGC 1158  
Db 1396 GATGAGTGAACCAAGAACCGAGTCAAGCTGACCTGCTGCTGCTCAAGGCTTCTATCCAGC 1455  
Qy 1159 GACATCGCGTGGAGTGGAGAGCAATGGGCGAGCGGAGAACCACTCAAGACCAACGCT 1218  
|||||

Db 1456 GACATCCCGTGGAGTGGGAGAGCAATGGCAGCGGAGAAACAACACTACAGACCAACGCT 1515  
Qy 1219 CCGTGTGACTCGAAGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGC 1278  
Db 1516 CCGTGTGACTCGAAGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGC 1575  
Qy 1279 AGTGGCAGCAGGAGGAGCTTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAAAC 1338  
Db 1576 AGTGGCAGCAGGAGGAGCTTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAAAC 1635  
Qy 1339 TACACGCAAGAGCCTCTCCCTGTCTCCGGTAAATGA 1377  
Db 1636 TACACGCAAGAGCCTCTCCCTGTCTCCGGTAAATGA 1674

RESULT 7

US-09-773-877B-19  
; Sequence 19, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 19  
; LENGTH: 1704  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flt1 (1-3 R->N) (Mut 4)  
; NAME/KEY: CDS  
; LOCATION: (1)..(1704)  
US-09-773-877B-19

Query Match 71.3%; Score 982.4; DB 4; Length 1704;  
Best Local Similarity 85.4%; Pred. No. 5.7e-253;  
Matches 1132; Conservative 0; Mismatches 161; Indels 33; Gaps 2;  
Qy 79 AGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATCCCGAAATATACATG 138  
Db 385 AGTGATACAGGTAGACCTTTCTGTAGAGATGTACAGTGAATCCCGAAATATACATG 444  
Qy 139 ACTGAAGGAAGGAGCTCGTCAITCCCTGCCGGGTACGTCACCTAAACATCACTGTTACT 198  
Db 445 ACTGAAGGAAGGAGCTCGTCAITCCCTGCCGGGTACGTCACCTAAACATCACTGTTACT 504  
Qy 199 TTAAGAAAGTTTCACATTGACACTTTGATCCCTGATGGAACCAATCTGGGACAGT 258  
Db 505 TTAAGAAAGTTTCACATTGACACTTTGATCCCTGATGGAACCAATCTGGGACAGT 564  
Qy 259 AGAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGCTTCTGACCTGTGAA 318  
Db 565 AGAAGGCTTCATCATATCAAAATGCAACGTACAAAGAAATAGGCTTCTGACCTGTGAA 624  
Qy 319 GCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCACATCGACAAACCAATACA 378  
Db 625 GCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCACATCGACAAACCAATACA 684  
Qy 379 ATCATAGATGGTTCGAGTCCGTCTCATGGAATTTGAATCTATCTGTTGGGAAAGCTT 438  
Db 685 ATCATAGATGGTTCGAGTCCGTCTCATGGAATTTGAATCTATCTGTTGGGAAAGCTT 744  
Qy 439 GTCTTAAATTTGACAGCAAGAACTGAATCTGAGGATTTGACTTCAACTGGGAATAC 498  
Db 745 GTCTTAAATTTGACAGCAAGAACTGAATCTGAGGATTTGACTTCAACTGGGAATAC 804  
Qy 499 CCTTCTTGAAGCATCAGCATAAGAACTTTGTAACCGAGACCTTAAACCCAGTCTGGG 558  
Db 805 CCTGATGAAAGAAATTAAGAACGCTTCCGTGAAGCGACGAATTTGACCAAGCAATTC--- 860  
|||||

Qy	559	AGTGAGATGAAGAAATTTTGGAGCACCTTAACTATAGATGGTGTAAACCCGGAGTGACCAA	618
Db	861	--CCATGCCAAACATATTTCTACAGTGTCTTACTATTGACAAAATGCAAGACAAA	918
Qy	619	GGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAGAAGAACACACATTTGTCT	678
Db	919	GGACTTTATACTTGTCTGTGTAAAGAGTGGACCATCATTTCAAATCTGTTAACACTCAGTG	978
Qy	679	AGGGTCCATGAAAA-----GGACAAAACTCACATATGC	711
Db	979	CATATATATGATAAAGCAGGCCCGGGGAGGCCCAAATCTTGTGACAAAACTCACATATGC	1038
Qy	712	CCACCGTGGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAA	771
Db	1039	CCACCGTGGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTTCTCTTCCCCCAAAA	1098
Qy	772	CCCAGGACACCTTCATGATCTCCGGACCCCTGGAGGTCAATGCGTGGTGGTGGACGTG	831
Db	1099	CCCAGGACACCTTCATGATCTCCGGACCCCTGGAGGTCAATGCGTGGTGGTGGACGTG	1158
Qy	832	AGGCACCAAGACCTGTAGGTCAGTTCAACTGGTACGTGACGGCGTGGAGGTGCATAT	891
Db	1159	AGGCACCAAGACCTGTAGGTCAGTTCAACTGGTACGTGACGGCGTGGAGGTGCATAT	1218
Qy	892	GCCAAGACAAGCCGCGGAGGACGACTCAACAGACAGTACCGTGTGGTCAGCGTCCCTC	951
Db	1219	GCCAAGACAAGCCGCGGAGGACGACTCAACAGACAGTACCGTGTGGTCAGCGTCCCTC	1278
Qy	952	ACGGTCTGTGCACAGGACTGGCTGAATGGCAAGAGTACAAGTGCAAGGTCTCCAAACAA	1011
Db	1279	ACGGTCTGTGCACAGGACTGGCTGAATGGCAAGAGTACAAGTGCAAGGTCTCCAAACAA	1338
Qy	1012	GCCTCCCGACCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA	1071
Db	1339	GCCTCCCGACCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCA	1398
Qy	1072	CAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACACAGGTTCAGCCTGACC	1131
Db	1399	CAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACACAGGTTCAGCCTGACC	1458
Qy	1132	TGGCTGTGTCAAGGCTTCTATCCAGCGCATCGCCGTGGAGTGGGAGAGCAATGGGCAG	1191
Db	1459	TGGCTGTGTCAAGGCTTCTATCCAGCGCATCGCCGTGGAGTGGGAGAGCAATGGGCAG	1518
Qy	1192	CCGAGAGAACACTACAAGACACAGCCTCCCGTGTCTGGACTCCGACGGCTCTTCTTCTCCTC	1251
Db	1519	CCGAGAGAACACTACAAGACACAGCCTCCCGTGTCTGGACTCCGACGGCTCTTCTTCTCCTC	1578
Qy	1252	TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAACGCTCTTCTCATGCTCC	1311
Db	1579	TACAGCAAGCTCACCGTGGACAGAGCAGGTGGCAGCAGGGGAACGCTCTTCTCATGCTCC	1638
Qy	1312	GTATGATCAGGGCTCTGCACCAACCTACACCCAGAAAGCCTCTCCCTGTCTCCGGGT	1371
Db	1639	GTATGATCAGGGCTCTGCACCAACCTACACCCAGAAAGCCTCTCCCTGTCTCCGGGT	1698
Qy	1372	AAATGA 1377	
Db	1699	AAATGA 1704	

## RESULT 8

US-09-773-877B-11  
; Sequence 11, Application US/09773877B  
; Patent No. 6833349  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710b  
; CURRENT APPLICATION NUMBER: US/09/773,877B  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0

QY 952 ACCGTCCTGCACAGGACTGCTGAATGGCAAGGATACAGTCAAGGTCTCCAAACAA 1011  
Db 1279 ACCGTCCTGCACAGGACTGCTGAATGGCAAGGATACAGTCAAGGTCTCCAAACAA 1338  
QY 1012 GCCCTCCAGAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1071  
Db 1339 GCCCTCCAGAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1398  
QY 1072 CAGGTGTACACCTGCGCCCATCCCGGGATGAGCTGACCAAGAACAGGTCAGCTGACC 1131  
Db 1399 CAGGTGTACACCTGCGCCCATCCCGGGATGAGCTGACCAAGAACAGGTCAGCTGACC 1458  
QY 1132 TGCTCTGCTCAAGGCTTCTATCCAGAGACATCCCGTGGAGTGGGAGCAATGGGCGAG 1191  
Db 1459 TGCTCTGCTCAAGGCTTCTATCCAGAGACATCCCGTGGAGTGGGAGCAATGGGCGAG 1518  
QY 1192 CCGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCCGACGGCTCTTCTCTC 1251  
Db 1519 CCGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCCGACGGCTCTTCTCTC 1578  
QY 1252 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCGAGCGGGAACGTCTTCTCATGTCTC 1311  
Db 1579 TACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCGAGCGGGAACGTCTTCTCATGTCTC 1638  
QY 1312 GTGATGATGAGGCTCTGCAACCACTTACACGCGAGAGAGCCTCTCCCTGTCTCCGGGT 1371  
Db 1639 GTGATGATGAGGCTCTGCAACCACTTACACGCGAGAGAGCCTCTCCCTGTCTCCGGGT 1698  
QY 1372 AAAAGA 1377  
Db 1699 AAAAGA 1704

## RESULT 9

US-08-227-496C-14

; Sequence 14, Application US/08227496C

; Patent No. 6130402

; GENERAL INFORMATION:

; APPLICANT: Greve, Jeffrey M.

; APPLICANT: McClelland, Alan

; TITLE OF INVENTION: Multimeric Forms of Human

; TITLE OF INVENTION: Rhinovirus Receptor Protein

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Bayer Corporation

; STREET: 400 Morgan Lane

; CITY: West Haven

; STATE: Connecticut

; COUNTRY: USA

; ZIP: 06516

; COMPUTER READABLE FORM:

; MEDIUM TYPE: diskette, 1.44 Mb storage

; COMPUTER: Dell Optiplex GX1

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect 8.0 for Windows

; CURRENT APPLICATION DATA:

; FILING DATE: 04/14/94

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/903,069

; FILING DATE: 06/22/92

; APPLICATION NUMBER: 07/704,984

; FILING DATE: 05/24/91

; APPLICATION NUMBER: 07/556,238

; FILING DATE: 07/20/90

; ATTORNEY/AGENT INFORMATION:

; NAME: Barbara A. Shimei

; REGISTRATION NUMBER: 29,862

; REFERENCE/DOCKET NUMBER: MTI 214.2C

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (203) 812-2786

TELEFAX: (203) 812-5492  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2043 bp  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: other nucleic acid  
; HYPOTHETICAL: no  
; ANTI-SENSE: no  
; FEATURE:  
; NAME/KEY: tICAM(453)/IgG fusion  
; OTHER INFORMATION: bp 1-1359 = nucleotides coding  
; OTHER INFORMATION: for amino acid residues 1-453 of ICAM-1; bp 1360-  
; OTHER INFORMATION: 2040 = nucleotides coding for amino acid residues  
; OTHER INFORMATION: 216-442 of human heavy chain IgG1; bp 2401-2043 =  
; OTHER INFORMATION: stop codon  
; US-08-227-496C-14

Query Match 49.8%; Score 686; DB 3; Length 2043;  
Best Local Similarity 95.9%; Pred. No. 1.6e-173;  
Matches 704; Conservative 0; Mismatches 30; Indels 0; Gaps 0;  
QY 644 GTGGGCTGATGACCAAGAAACAGACACATTTGTGAGGGTCCATGAAAGGACAAAACTC 703  
Db 1310 GGAGAGTACCCGCAAGGTGACCGTGNATGTCTCTCCCCCGGTATGAGGACAAAACTC 1369  
QY 704 ACATATGCCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCACTTTCTCTTCC 763  
Db 1370 ACATATGCCACCGTCCCGAGCACCTGAACTCTCTGGGGGACCGTCACTTTCTCTTCC 1429  
QY 764 CCCCAGAACCCAGAGCACCCCTCATGATCTCCCGGACCCCTGAGGTACATGGGTGGTGG 823  
Db 1430 CCCCAGAACCCAGAGCACCCCTCATGATCTCCCGGACCCCTGAGGTACATGGGTGGTGG 1489  
QY 824 TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGG 883  
Db 1490 TGGACGTGAGCCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGAGCGGTGGAGG 1549  
QY 884 TGATATGCAAGACAAAGCCCGGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGTGCA 943  
Db 1550 TGATATGCAAGACAAAGCCCGGGAGGAGCAGTACAAAGCAGCAGTACCGGTGTGTGCA 1609  
QY 944 GCCTCTCACCGTCTGACACGAGCTGCTGATGCAAGAGGAGTACAAAGTCAAGTCT 1003  
Db 1610 GCCTCTCACCGTCTGACACGAGCTGCTGATGCAAGAGGAGTACAAAGTCAAGTCT 1669  
QY 1004 CCAACAAAGCCCTCCAGAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1063  
Db 1670 CCAACAAAGCCCTCCAGAGCCCATCGAGAAACCATCTCCAAAGCCAAAGGGCAGCCCC 1729  
QY 1064 GAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGTGAACCAAGACCCAGTCA 1123  
Db 1730 GAGAACACAGGTGTACACCTGCCCCCATCCCGGGATGAGTGAACCAAGACCCAGTCA 1789  
QY 1124 GCCTGACCTGCTGTCAGAGGCTTCTATCCAGCAGCATCGCGGTGAGTGGGAGAGCA 1183  
Db 1790 GCCTGACCTGCTGTCAGAGGCTTCTATCCAGCAGCATCGCGGTGAGTGGGAGAGCA 1849  
QY 1184 ATGGGAGCCCGGAGAACCAACTACAAGACCAACGCTCCCGTGTGCTGGAATCCGACCGCTCT 1243  
Db 1850 ATGGGAGCCCGGAGAACCAACTACAAGACCAACGCTCCCGTGTGCTGGAATCCGACCGCTCT 1909  
QY 1244 TCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGCGGTGGCAGCAGGGGAAACGTCTTCT 1303  
Db 1910 TCTTCTCTTACAGCAAGCTCACCGTGGACAAGAGCGGTGGCAGCAGGGGAAACGTCTTCT 1969  
QY 1304 CATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGAGAGAGGCTCTCCCTGT 1363  
Db 1970 CATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGAGAGAGGCTCTCCCTGT 2029  
QY 1364 CTCGGGTAAATGA 1377  
|||||

Db 2030 CTCGGGTAATGA 2043

RESULT 10  
US-09-023-655-1223  
; Sequence 1223, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREMITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1223:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 705 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g243865  
US-09-023-655-1223

Query Match 49.7%; Score 684; DB 4; Length 705;  
Best Local Similarity 100.0%; Pred. No. 3.4e-173;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCACCGTGCAGCACCCTGAACTCTCTGGGGGACCGTCAGTC 753  
DB 5 GACAAACTCACATGCCACCGTGCAGCACCCTGAACTCTCTGGGGGACCGTCAGTC 64

QY 754 TTCTCTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTGACA 813  
DB 65 TTCTCTCTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTGACA 124

QY 814 TGCGTGCGTGGTAGCGTAGCCACGAAGCCCTGAGGTCAAGTTCAACTGGTAGCTGGAC 873  
DB 125 TGGCGTGGTGGAGCTGAGGCCAAGAACCCTGAGGTCAAAGTTCAAAGTGGTAGCTGGAC 184

QY 874 GGCGTGAGGTGCATAATSCCAAGAACCGCGGGAGGAGCAGTCAACACAGACACCTAC 933  
DB 185 GGGCGTGAGGTGCATAATGCCAAGAACAAAGCCGCGGGAGGAGCAGTCAACACAGCACCTAC 244

QY 934 CGTGTGGTCAAGGTCTCTCACCGTCTCGACACGAGTCTGGCTGAATGGCAAGGAGTACAAG 993

Db 245 CGTGTGGTCAAGGTCTCTCACCGTCTCGACACAGGACTGGCTGAATGGCAAGGAGTACAAG 304

QY 994 TGCRAAGGTCTCCAACAAAAGCCCTCCCAGACCCCATCGAGAAAAACCATCTCCAAGGCCAAA 1053

Db 305 TGCRAAGGTCTCCAACAAAAGCCCTCCCAGACCCCATCGAGAAAACCATCTCCAAGGCCAAA 364

QY 1054 GGGCAGACCCCGAGAACCAACAGGTGTACACCTTGCCCCCATCCCGGGNATAGCTGACCAAG 1113

Db 365 GGGCAGACCCCGAGAACCAACAGGTGTACACCTTGCCCCCATCCCGGGNATAGCTGACCAAG 424

QY 1114 AACCAAGTCAAGCTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCCCGGTGGAG 1173

Db 425 AACCAAGTCAAGCTGACCTGCTGGTCAAAAGGCTTCTATCCAGCGACATCCCGGTGGAG 484

QY 1174 TGGGAGAGCAATGGGACGCCGAGAACCAACTACAAGACCAACGCTCCCGTGGCTGGACTCC 1233

Db 485 TGGGAGAGCAATGGGACGCCGAGAACCAACTACAAGACCAACGCTCCCGTGGCTGGACTCC 544

QY 1234 GACGGCTCTCTTCTCTTACAGCAAGCTCAACGTTGGACAAGAGCAGGTTGGCAGCAGGGG 1293

Db 545 GACGGCTCTCTTCTCTTACAGCAAGCTCAACGTTGGACAAGAGCAGGTTGGCAGCAGGGG 604

QY 1294 AACGTTCTCTATGCTCCGTTGATGATGAGGCTCTGCAACCACTACACGCGAAGAGC 1353

Db 605 AACGTTCTCTATGCTCCGTTGATGATGAGGCTCTGCAACCACTACACGCGAAGAGC 664

QY 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377

Db 665 CTCTCCCTGTCTCCGGGTAAATGA 688

RESULT 11  
US-09-178-869-1  
; Sequence 1, Application US/09178869B  
; Patent No. 6197294  
; GENERAL INFORMATION:  
; APPLICANT: Tao, Weng  
; APPLICANT: Wong, Shou  
; APPLICANT: Hickey, William F.  
; APPLICANT: Hamman, Joseph P.  
; APPLICANT: Baetge, E. Edward  
; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION  
; FILE REFERENCE: 17810-043  
; CURRENT APPLICATION NUMBER: US/09/178,869B  
; CURRENT FILING DATE: 1998-10-26  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 1019  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: gene  
; LOCATION: (..)  
; OTHER INFORMATION: Description of Sequence: Recombinant  
; OTHER INFORMATION: Polynucleotide  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (16)...(1008)  
US-09-178-869-1

Query Match 49.7%; Score 684; DB 3; Length 1019;  
Best Local Similarity 100.0%; Pred. No. 4e-173;  
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCACCGTGCAGCACCCTGAACTCTCTGGGGGACCGTCAGTC 753  
DB 328 GACAAACTCACATGCCACCGTGCAGCACCCTGAACTCTCTGGGGGACCGTCAGTC 387

QY 754 TTCTCTCTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTGACA 813  
DB 388 TTCTCTCTCCCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTGACA 447



Qy	814	TGCGTGTGTGTGGAGCGCAGAGACCCTGAGGTCAAGTTCAACTGTGTCAGTGAC	873
Db	448	TGCGTGTGTGTGGAGCGCGTAGCAGCAGAGACCCTGAGTCAAGTTCAA	507
Qy	874	GGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGGGAGGAGCAGTACAA	933
Db	508	GGCGTGGAGGTGCATAATGCCAAGCAAAAGCCGGGAGGAGCAGTACAA	567
Qy	934	CGTGTGGTACGCGTCTCAACGTCCTGCACACGAGACTGGCTGAATGCAAGGAGTACAAG	993
Db	568	CGTGTGGTACGCGTCTCAACGTCCTGCACACGAGACTGGCTGAATGCAAGGAGTACAAG	627
Qy	994	TGCAAGGTCTCCAAACAAAGCCCTCCAGCGCCCCATCGAGAAAAACATCTCCAAAGCCAAA	1053
Db	628	TGCAAGGTCTCCAAACAAAGCCCTCCAGCGCCCCATCGAGAAAAACATCTCCAAAGCCAAA	687
Qy	1054	GGGCAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAG	1113
Db	688	GGGCAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGGATGAGCTGACCAAG	747
Qy	1114	AACCAAGTTCAGCCTGACCTGCTGGTCAAGGCTTCTATCCAGGGACATGCCGCTGGAG	1173
Db	748	AACCAAGTTCAGCCTGACCTGCTGGTCAAGGCTTCTATCCAGGGACATGCCGCTGGAG	807
Qy	1174	TGGGAGAGCAATGGGACGCGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCC	1233
Db	808	TGGGAGAGCAATGGGACGCGGAGAACAACTACAAGACCAACGCTCCCGTGTGGACTCC	867
Qy	1234	GACGGCTCTTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG	1293
Db	868	GACGGCTCTTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGCAGGGG	927
Qy	1294	AACGTCCTTCTCATGCTCCGTGATGCATGAGGCTGTGCACAAACCACTACACGAGAAGAGC	1353
Db	928	AACGTCCTTCTCATGCTCCGTGATGCATGAGGCTGTGCACAAACCACTACACGAGAAGAGC	987
Qy	1354	CTCTCCCTGTCTCCGGGTAAATGA	1377
Db	988	CTCTCCCTGTCTCCGGGTAAATGA	1011

Query Match	49.7%; Score 584; DB 4; Length 1019;
Best Local Similarity	100.0%; P:indels; 0; Mismatches 0; Gaps 0;
Matches 684; Conservative 0;	
QY	694 GACAAACTCACACATGCCACCGTGGCCAGCAGCTGAATCTCTGGGGGACCGTCAAGTC 753
DB	328 GACAAAACTCACACATGCCACCGTGGCCAGCAGCTGAATCTCTGGGGGACCGTCAAGTC 387
QY	754 TTCCTCTTCCCCCAAAACCAAGGACACCTCTCATGATCTCCCGAGCCCTCTAGAGTCACA 813
DB	388 TTCCTCTTCCCCCAAAACCAAGGACACCTCTCATGATCTCCCGAGCCCTCTAGAGTCACA 447
QY	814 TGGCTGTGTGGAGCTGAGACGACGAAAGACCCCTGAGGTCAAAGTTCAAATGGTACGTGGAC 873
DB	448 TGGCTGTGTGTGGAGCTGAGACGACGAAAGACCCCTGAGGTCAAAGTTCAAATGGTACGTGGAC 507
QY	874 GGGCTGTGAGTGGCATATGCGNAGACAAAGCCGCGGAGGAGCAGTACACACGACGTCAC 933
DB	508 GGGCTGTGAGTGGCATATGCGNAGACAAAGCCGCGGAGGAGCAGTACACACGACGTCAC 567
QY	934 CGTGTGCTCAGCGTCTCACCGTCTCTGCACACAGGACTGGCTGAATGCAAGGAGTACAAG 993
DB	568 CGTGTGCTCAGCGTCTCACCGTCTCTGCACACAGGACTGGCTGAATGCAAGGAGTACAAG 627
QY	994 TGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATGAGAAAAACCATCTCCAAAGCCAAA 1053
DB	628 TGCAGGTCTCCAAACAAAGCCCTCCAGCCCCCATGAGAAAAACCATCTCCAAAGCCAAA 687
QY	1054 GGGCAGCCCCGAGNACACAGGTGTACACCTGCCCCCATCCCGGAGTGAAGTACCAAG 1113
DB	688 GGGCAGCCCCGAGNACACAGGTGTACACCTGCCCCCATCCCGGAGTGAAGTACCAAG 747
QY	1114 AACCAGGTTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG 1173
DB	748 AACCAGGTTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCCGTGGAG 807
QY	1174 TGGGAGAGCAATGGGCGAGCCGAGAAACAACTACAAGACCAAGCTCCCGTGTGGACTCC 1233
DB	808 TGGGAGAGCAATGGGCGAGCCGAGAAACAACTACAAGACCAAGCTCCCGTGTGGACTCC 867
QY	1234 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGTGGCAGCAGGG 1293
DB	868 GACGGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGTGGCAGCAGGG 927
QY	1294 AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGC 1353
DB	928 AACGTCTTCTCATGCTCCGTGATGATGAGGCTCTGCACAAACCACTACACGCAAGAGC 987
QY	1354 CTCTCCCTGTCTCGGTTAAATGA 1377
DB	988 CTCTCCCTGTCTCGGTTAAATGA 1011
RESULT 13	
US-09-180-100-18	
; Sequence 18, Application US/09180100	
; Patent No. 6306395	
; GENERAL INFORMATION:	
; APPLICANT: NAKAMURA, No. 6306395io	
; APPLICANT: NAGATA, Shigekazu	
; TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE	
; FILE REFERENCE: 1110-207P	
; CURRENT APPLICATION NUMBER: US/09/180,100	
; CURRENT FILING DATE: 1998-11-02	
; EARLIER APPLICATION NUMBER: PCT/JF97/01502	
; EARLIER FILING DATE: 1997-05-01	
; NUMBER OF SEQ ID NOS: 25	
; SOFTWARE: PatentIn Ver. 2.0	
; SEQ ID NO 18	
; LENGTH: 1182	
; TYPE: DNA	
; ORGANISM: Homo sapiens	
US-09-180-100-18	

```
Query Match          49.7%; Score 684; DB 3; Length 1182;
Best Local Similarity 100.0%; Pred. No. 4.2e-173;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATATGCGCCAGCCAGTCCAGCACTCTCTGGGGGACCGTCAGTC 753
Db 483 GACAAACTCACATATGCGCCAGCCAGTCCAGCACTCTCTGGGGGACCGTCAGTC 542

QY 754 TTCTCTTCCCTCCAAACCCAGGACACCTCATGATCTCCGGGACCCCTGAGTCA 813
Db 543 TTCTCTTCCCTCCAAACCCAGGACACCTCATGATCTCCGGGACCCCTGAGTCA 602

QY 814 TCGTGGTGGTGGAGCGTGGAGCCAGCAACGACCTTGAGGTCAAGTTCAGTGGTGGAC 873
Db 603 TCGTGGTGGTGGAGCGTGGAGCCAGCAACGACCTTGAGGTCAAGTTCAGTGGTGGAC 562

QY 874 GCGTGGAGGTGATATATCCAAAGACAAAGCCCGGGAGGAGCAGTACAAACGACGTAC 933
Db 663 GCGTGGAGGTGATATATCCAAAGACAAAGCCCGGGAGGAGCAGTACAAACGACGTAC 722

QY 934 CGTGTGGTGGAGTCTCAGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 993
Db 723 CGTGTGGTGGAGTCTCAGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 782

QY 994 TGCAAGGTCTCCAAACCCAGGACACCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCCAAA 1053
Db 783 TGCAAGGTCTCCAAACCCAGGACACCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCCAAA 842

QY 1054 GGGAGAGCCCGAGAACCCAGAGTGTACACCTGCCCCCCTCCAGGATGAGTCAACCAAG 1113
Db 843 GGGAGAGCCCGAGAACCCAGAGTGTACACCTGCCCCCCTCCAGGATGAGTCAACCAAG 902

QY 1114 AACGAGTCAAGTCAAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 1173
Db 903 AACGAGTCAAGTCAAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCCAG 962

QY 1174 TGGGAGAGCAATGGGCGAGCGGAGAACCACTACAGACCAACGACCTCCCGTGTGGACTCC 1233
Db 963 TGGGAGAGCAATGGGCGAGCGGAGAACCACTACAGACCAACGACCTCCCGTGTGGACTCC 1022

QY 1234 GACGAGTCTCTTCTCTTACAGCAAGTCAACGTTGAGGAGCAAGAGAGTGGCAGAGGG 1293
Db 1023 GACGAGTCTCTTCTCTTACAGCAAGTCAACGTTGAGGAGCAAGAGAGTGGCAGAGGG 1082

QY 1294 AACGTTCTTCTATGCTCCGTTGATGATGAGGCTCTGCAACCACTACAGCAGAGAGC 1353
Db 1083 AACGTTCTTCTATGCTCCGTTGATGATGAGGCTCTGCAACCACTACAGCAGAGAGC 1142

QY 1354 CTCTCCCTCTCTCCGGTAAATGA 1377
Db 1143 CTCTCCCTCTCTCCGGTAAATGA 1166
```

```
RESULT 14
US-08-488-376-19
; Sequence 19, Application US/08488376
; Patent No. 5811524
; GENERAL INFORMATION:
; APPLICANT: CHAMAT, Peter
; APPLICANT: BRAMS, Soulaime Salim
; APPLICANT: PAN, Li-Zhen
; APPLICANT: WALSH, Edward E.
; APPLICANT: HEARD, Cheryl Janne
; APPLICANT: NEWMAN, Roland Anthony
; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND
; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
```

```
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,376
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-150
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1428 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1428
US-08-488-376-19
```

```
Query Match          49.7%; Score 684; DB 1; Length 1428;
Best Local Similarity 100.0%; Pred. No. 4.6e-173;
Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 694 GACAAACTCACATGCCCCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAGTC 753
Db 745 GACAAACTCACATGCCCCACCGTGGCCAGCACCTGAACTCTCTGGGGGACCGTCAGTC 804

QY 754 TTCTCTTCCCTCCAAACCCAGGACACCTCATGATCTCCGGGACCCCTGAGTCA 813
Db 805 TTCTCTTCCCTCCAAACCCAGGACACCTCATGATCTCCGGGACCCCTGAGTCA 864

QY 814 TCGTGGTGGTGGAGCGTGGAGCCAGACCTCTGAGGTCAAGTTCACTGGTGGAC 873
Db 865 TCGTGGTGGTGGAGCGTGGAGCCAGACCTCTGAGGTCAAGTTCACTGGTGGAC 924

QY 874 GCGTGGAGGTGTCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTC 933
Db 925 GCGTGGAGGTGTCATAATGCCAAGACAAAGCCCGGGAGGAGCAGTACAAACAGCAGTC 984

QY 934 CGTGTGGTGGAGTCTCTCAGCGTCTGACACAGAGTGGCTGAATGGCAAGGAGTACAG 993
Db 985 CGTGTGGTGGAGTCTCTCAGCGTCTGACACAGAGTGGCTGAATGGCAAGGAGTACAG 1044

QY 994 TGCAAGGTCTCCAAACCCAGGACACCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCCAAA 1053
Db 1045 TGCAAGGTCTCCAAACCCAGGACACCTCCAGCCCGCCATCGAGAAACCATCTCCAAAGCCAAA 1104

QY 1054 GGGCAGCCCGGAGAACCAACAGGTGTACACCTTGCCCCCATCCCGGGATGAGTCAACCAAG 1113
Db 1105 GGGCAGCCCGGAGAACCAACAGGTGTACACCTTGCCCCCATCCCGGGATGAGTCAACCAAG 1164

QY 1114 AACAGGTGAGCTGACCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1173
Db 1165 AACAGGTGAGCTGACCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1224

QY 1174 TGGGAGAGCAATGGGCGAGCGGAGAACCACTACAGAGCACGCTCCCGTCTGAGTCC 1233
Db 1225 TGGGAGAGCAATGGGCGAGCGGAGAACCACTACAGAGCACGCTCCCGTCTGAGTCC 1284

QY 1234 GACGCTCTCTTCTCTCTACAGCAAGCTCACCGTGGCAAGAGCAGGTGGCAGCAGGG 1293
```

Db 1285 GACGCTCTTCTTCTCTACAGCAAGCTCACCGTGGACAAGAGCAGGTGGCAGAGGG 1344

Qy 1294 AACGTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAACCACTACTACCCAGAAGGC 1353

Db 1345 AACGTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAACCACTACTACCCAGAAGGC 1404

Qy 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377

Db 1405 CTCTCCCTGTCTCCGGGTAAATGA 1428

RESULT 15

US-08-634-223-19

; Sequence 19, Application US/08634223

; Patent No. 5840298

; GENERAL INFORMATION:

; APPLICANT: BRAMS, Peter

; APPLICANT: CHAMAT, Soulaïma Salim

; APPLICANT: PAN, Li-Zhen

; APPLICANT: WALSH, Edward E.

; APPLICANT: HEARD, Cheryl Janne

; APPLICANT: NEWMAN, Roland Anthony

; TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN

; TITLE OF INVENTION: MONOCLONAL ANTIBODIES SPECIFIC TO RSV F-PROTEIN AND

; TITLE OF INVENTION: METHODS FOR THEIR MANUFACTURE AND THERAPEUTIC USE THEREOF

; NUMBER OF SEQUENCES: 19

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P.O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/634,223

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/488,376

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/POCKET NUMBER: 012712-150

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 19:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1428 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 1..1428

US-08-634-223-19

Query Match 49.7%; Score 684; DB 2; Length 1428;

Best Local Similarity 100.0%; Pred.No. 4.6e-173;

Matches 684; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 694 GACAAAACCTCACACTGCCACCGTGGCCACGACCTGAACTCTTGGGGGGACCGTCAGTC 753

Db 745 GACAAAACCTCACACTGCCACCGTGGCCACGACCTGAACTCTTGGGGGGACCGTCAGTC 804

Qy 754 TTCTCTTCTCCCAAAACCCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCA 813

Db 805 TTCTCTTCTCCCAAAACCCAAAGACACCTCTATGATCTCCCGGACCCCTGAGTCA 864

Qy 814 TGGTGTGTGTGAGCGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 873

Db 865 TGGTGTGTGTGAGCGTGAGCCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGTGGAC 924

Qy 874 GGGTGTGAGGTGTCATANTGCCAAGAACGCGGGGAGGAGCAGTACAACGACACGTAC 933

Db 925 GGGTGTGAGGTGTCATANTGCCAAGAACGCGGGGAGGAGCAGTACAACGACACGTAC 984

Qy 934 CGTGTGTGTCAGCGTCTCTCACCGTCTCTGCACAGGACTGGCTGTAATGCAAGGAGTACAAG 993

Db 985 CGTGTGTGTCAGCGTCTCTCACCGTCTCTGCACAGGACTGGCTGTAATGCAAGGAGTACAAG 1044

Qy 994 TGCAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAAACCATCTCCAAAGCCAAA 1053

Db 1045 TGCAAGGTCTCCAAACAAAGCCCTCCAGCCGCCCATCGAGAAAACCATCTCCAAAGCCAAA 1104

Qy 1054 GGGCAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1113

Db 1105 GGGCAGCCCGAGAACCAACAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAG 1164

Qy 1114 AACGAGTTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCGCTGGAG 1173

Db 1165 AACGAGTTCAGCCTGACCTGCTGGTCAAAGGCTTCTATCCAGCGACATCGCGCTGGAG 1224

Qy 1174 TGGGAGAGCAATGGGCGAGCCGAGAACAACTACAAGACCAAGCTCCCGTGTGGACTCC 1233

Db 1225 TGGGAGAGCAATGGGCGAGCCGAGAACAACTACAAGACCAAGCTCCCGTGTGGACTCC 1284

Qy 1234 GAGGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGG 1293

Db 1285 GAGGGCTCTCTTCTCTACAGCAAGCTCACCGTGGACAAAGAGCAGGTGGCAGCAGGG 1344

Qy 1294 AACGTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAACCACTACAGCGAGAAGGC 1353

Db 1345 AACGTCTTCTCATGCTCCGCTGATGATGAGGCTCTGCACAACCACTACAGCGAGAAGGC 1404

Qy 1354 CTCTCCCTGTCTCCGGGTAAATGA 1377

Db 1405 CTCTCCCTGTCTCCGGGTAAATGA 1428

Search completed: August 27, 2005, 10:45:54

Job time : 253.401 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 26, 2005, 22:22:41 / Search time 960.42 Seconds  
(without alignments)  
9381.136 Million cell updates/sec

Title: US-10-009-852-15  
Perfect score: 1377  
Sequence: 1 atggtcagctactgggacac.....ccctgtctccgggtaaatga 1377

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7331713 seqs, 3271544945 residues  
Total number of hits satisfying chosen parameters: 14663426

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US05\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US10G\_PUBCOMB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US10H\_PUBCOMB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US10I\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
23: /cgn2\_6/ptodata/2/pubpna/US11A\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1377	100.0	1377	10	US-09-773-877A-25
2	1377	100.0	1377	17	US-10-609-775-9
3	1377	100.0	1377	20	US-10-860-958-1
4	1377	100.0	1377	21	US-10-830-902-1
5	1377	100.0	1377	21	US-10-897-802-1
6	1377	100.0	1377	21	US-10-880-021-9
7	1377	100.0	1377	21	US-10-909-011-3

RESULT 1  
US-09-773-877A-25  
; Sequence 25, Application US/09773877A  
; Publication No. US20030017977A1  
; GENERAL INFORMATION:  
; APPLICANT: Xia, Yu-Ping et al.  
; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATORY SKIN DISEASES  
; FILE REFERENCE: REG 710B  
; CURRENT APPLICATION NUMBER: US/09/773.877A  
; CURRENT FILING DATE: 2001-01-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 25  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: VEGFR1R2.FcdeltaC1(a) Receptor  
; NAME/KEY: CDS  
; LOCATION: (1)..(1377)  
US-09-773-877A-25

Query Match 100.0%; Score 1377; DB 10; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGTCTCAGCTGCTGCTTC 60  
Db 1 ATGTCAGCTACTGGGACACCGGGGTCTGCTGTGCGCGTCTCAGCTGCTGCTTC 60

Sequence 15, Appl  
Sequence 15, Appl  
Sequence 21, Appl  
Sequence 7, Appl  
Sequence 1, Appl  
Sequence 11, Appl  
Sequence 12, Appl  
Sequence 23, Appl  
Sequence 12, Appl  
Sequence 12, Appl  
Sequence 13, Appl  
Sequence 13, Appl  
Sequence 15, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 17, Appl  
Sequence 7, Appl  
Sequence 7, Appl  
Sequence 13, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 19, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 11, Appl  
Sequence 1, Appl  
Sequence 1, Appl  
Sequence 7, Appl  
Sequence 9, Appl  
Sequence 9, Appl  
Sequence 31, Appl  
Sequence 29, Appl  
Sequence 27, Appl  
Sequence 23, Appl

ALIGNMENTS

Qy	61	ACAGGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC	120
Db	61	ACAGGATCTAGTTCGCGAAGTGATACCGGTAGACCTTTCTGTAGAGATGTACAGTGAATC	120
Qy	121	CCCGAAATATACACATGACTGAAGGAGGAGCTCGTCACTTCCTCCCGGTTACGTCA	180
Db	121	CCCGAAATATACACATGACTGAAGGAGGAGCTCGTCACTTCCTCCCGGTTACGTCA	180
Qy	181	CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTTGATGCCCTGTAGTGA	240
Db	181	CCTAACATCACTGTTACTTTAAAAAAGTTTCCACTTGACACTTTTGATGCCCTGTAGTGA	240
Qy	241	CGCATAATCTGGGACGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA	300
Db	241	CGCATAATCTGGGACGTAGAAAGGGCTTCATCATATCAAATGCAACGTACAAAGAAATA	300
Qy	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATATAGACAAACTATCTCA	360
Db	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCATTTGTATATAGACAAACTATCTCA	360
Qy	361	CATCGACAAACCAATACAATCATAGATGTGGTCTCTGAGTCGGTCTCATGGAATTGA	420
Db	361	CATCGACAAACCAATACAATCATAGATGTGGTCTCTGAGTCGGTCTCATGGAATTGA	420
Qy	421	TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTAACAGCAAGAACTGAACATAAATGTGGG	480
Db	421	TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTAACAGCAAGAACTGAACATAAATGTGGG	480
Qy	481	GACTTCAACTGGGAATACCTCTTTCGAAAGCATCAGCATAGAAGAACTGTGAACCGG	540
Db	481	GACTTCAACTGGGAATACCTCTTTCGAAAGCATCAGCATAGAAGAACTGTGAACCGG	540
Qy	541	CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAAATTTTGTGACACTTAACTATAGAT	600
Db	541	CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAAATTTTGTGACACTTAACTATAGAT	600
Qy	601	GTAACCCGGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGCTGATGAC	660
Db	601	GTAACCCGGAGTGACCAAGGATTTGTACACCTGTGCAGCATCCAGTGGCTGATGAC	660
Qy	661	AAGAACAGCATTTTGTGACGGTCCATGAAGAGCAAACTCAACATGCCCAACGTGC	720
Db	661	AAGAACAGCATTTTGTGACGGTCCATGAAGAGCAAACTCAACATGCCCAACGTGC	720
Qy	721	CCACACTGAACCTCTGGGGGACCGTCAGTCTTCTTCTCCCCCAAACCCAAGGAC	780
Db	721	CCACACTGAACCTCTGGGGGACCGTCAGTCTTCTTCTCCCCCAAACCCAAGGAC	780
Qy	781	ACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTGAGCCAG	840
Db	781	ACCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTGAGCCAG	840
Qy	841	GACCTGAGGTCAGGTTCAACTGTGACGGCGTGGAGGTGCATTAATGCCAAGACA	900
Db	841	GACCTGAGGTCAGGTTCAACTGTGACGGCGTGGAGGTGCATTAATGCCAAGACA	900
Qy	901	AAGCCGGGGAGGACAGTACAAAGCAACGTACCGTGTGGTCAAGGCTCTCACCGT	960
Db	901	AAGCCGGGGAGGACAGTACAAAGCAACGTACCGTGTGGTCAAGGCTCTCACCGT	960
Qy	961	CACCAGGACTGGCTGAATGGCAAGGATCAAGTGCAAGGTCTCCAAAGAGCCCTCCA	1020
Db	961	CACCAGGACTGGCTGAATGGCAAGGATCAAGTGCAAGGTCTCCAAAGAGCCCTCCA	1020
Qy	1021	GCCCCCATCGAGAAAAACATCTCCAAAGCCAAAGGACGCCGCCAGAACCAAGGTGT	1080
Db	1021	GCCCCCATCGAGAAAAACATCTCCAAAGCCAAAGGACGCCGCCAGAACCAAGGTGT	1080
Qy	1081	ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTCAAGCTGACCTGGT	1140
Db	1081	ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGGTCAAGCTGACCTGGT	1140
Qy	1141	AAAGGCTTCTATCCAGCGCATCGCCGTGGAGTGGGAGAGCAATGGCAGCCGAGAAC	1200

## RESULT 2

US-10-609-775-9

09-10-003-773-5  
; Sequence 9, Application US/10609775

Publication No. US20040014667A1

; PUBLICATION NO: 0020  
; GENERAL INFORMATION:

: APPLICANT: Thomas J. Daly

APPLICANT: James P. Fandl

APPLICANT: Nicholas J. Papadopoulos

; TITLE OF INVENTION: VEGF

; FILE REFERENCE: REG 710D

; CURRENT APPLICATION NUMBER: US/1

;  
; CURRENT FILING DATE: 2003-06-30

;  
PRIOR APPLICATION NUMBER: 10/

; PRIOR FILING DATE: 2001-12-06

; PRIOR APPLICATION NUMBER: PCT

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/

PRIOR FILING DATE: 1999-06-08

```

; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0

```

; SOFTWARE: FAS  
: SEQ ID NO 9

```

; SEQ ID NO 9
:      LENGTH: 1377

```

```

; LENGTH: 1.
; TYPE: DNA

```

```

; TYPE: DNA
; ORGANISM: homo sapiens

```

US-10-609-775-9

Query Match 100.0%: Score 1377: DB 17: Length 1377:

Query Match:	100.0%;	Score 1577;
Best Local Similarity	100.0%;	Pred. No. 0;

Best local similarity 100.0%, rec. no: 0,  
Matches 1377: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

1 ATGGTCAGGCTA CTGGGACACCGGGTCTGTGTGGGGCTGCTCAGCTGTCTGCTCTC 60

[illegible]

DD T AIGGTCAGGCTAC TGGGACHACCGGGATCC TGTGTGGGCTGCTCAGCTATGCTTCTC 80

QV 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

Dh 61 ACAGGATCTAGTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAAATC 120

DD 6T ACAGGATCTAGTTC CGAAGTGA TACCGGTAGACCTTTCGTAGAGAGTGTACACGTGAAATC 120

QY 121 CCCGATAATATACACAATGACCTGAAGGHAAGGGAGCTCGTCATCTCCCTGCGGCTACGGTCA 180

Db 121 CCGGAAATTATACATGACTGAAGGAAGGAGGTCCTCGTCA TTCCCTGCCGGGTACGTCA 180

Q17 181 CCTAACATCATCTGTTACTTTAAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAAA 240

QY CCIAHCAIACACIGIACIIATAATAAGIITCCACIIGHACACIITGATCCCGATGGAGATA 240  
TBT

DB 181 CCCTAACATCACCTGTACTTCTAAATAAGTTTCCACCTTGACACCTTGTATCCCTGATGGAAAA 240

241 CGCATAATCTGGGACAGTAGAAACGGCTTCATCATATCAAAATGCAACGTCACAAAGAAATA 300

241 C C C A T A T A T C T C C C A C A C T A C A A C G T A C A A C A A T A 300

DB 241 CGCATAAATCTGGGACAGTAGAAAGGGCTTCATTCATATCATAATGCATACGTCACATAGATAATA 300

421 TCCTGTTGGAGAAAGCTTCTCTTAATAATTGTACAGCAAGAACTGAACCTAAATGTGGGATTT 480  
421 TCCTGTTGGAGAAAGCTTCTCTTAATAATTGTACAGCAAGAACTGAACCTAAATGTGGGATTT 480  
481 GACTTCACTGGGATACCTCTTCGAGAGCATCAGCAAGAACTTTGTAACCCAGAC 540  
481 GACTTCACTGGGATACCTCTTCGAGAGCATCAGCAAGAACTTTGTAACCCAGAC 540  
541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600  
541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600  
601 GTAACCCGAGTGACCAAGATTTGTACACCTGTGCGAGCATCCAGTGGGCTGATGACCAAG 660  
601 GTAACCCGAGTGACCAAGATTTGTACACCTGTGCGAGCATCCAGTGGGCTGATGACCAAG 660  
661 AAGAACAGCAGATTTGTACGGGTCCATGAAAGAGCAAAACTCACACATGCCACCGTGC 720  
661 AAGAACAGCAGATTTGTACGGGTCCATGAAAGAGCAAAACTCACACATGCCACCGTGC 720  
721 CCAGCACCTGAACTCTCGGGGGACCGTCAGTCTTCTTCCCTCCCAAAACCCCAAGGAC 780  
721 CCAGCACCTGAACTCTCGGGGGACCGTCAGTCTTCTTCCCTCCCAAAACCCCAAGGAC 780  
781 ACCCTCATGATCTCCCGGACCCCTCAGGTTCACATCGTGTGGTGGAGCGTGAGCCACGAA 840  
781 ACCCTCATGATCTCCCGGACCCCTCAGGTTCACATCGTGTGGTGGAGCGTGAGCCACGAA 840  
841 GACCTGAGGTCAAGTTCACTGTTGAGAGCGGTGAGGTGCAATATGCCAAGACA 900  
841 GACCTGAGGTCAAGTTCACTGTTGAGAGCGGTGAGGTGCAATATGCCAAGACA 900  
901 AAGCCGCGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGGTGGAGCGTCTCACCGTCTG 960  
901 AAGCCGCGGAGGAGCAGTACAAAGCAGCAGTACCGTGTGGTGGAGCGTCTCACCGTCTG 960  
961 CACCAAGGACTGGCTGAAATGGCAAGGAGTACAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1020  
961 CACCAAGGACTGGCTGAAATGGCAAGGAGTACAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1020  
1021 GCCCCATCGAGAAACCATCTCCAAAGCAGGAGTGAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1080  
1021 GCCCCATCGAGAAACCATCTCCAAAGCAGGAGTGAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1080  
1081 ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1140  
1081 ACCTGCCCCCATCCCGGATGAGCTGACCAAGAACCAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1140  
1141 AAAGGCTTCTATCCAGCGCATCCCGGATGAGCTGACCAAGAACCAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1200  
1141 AAAGGCTTCTATCCAGCGCATCCCGGATGAGCTGACCAAGAACCAAGTGCAGGTCTCCCAAAAGGCGCTCCCA 1200  
1201 AACTACAAGACCAAGCTCCCGTGTGAGTCCCGAGCGGTCTTCTTCTCTACAGCAAG 1260  
1201 AACTACAAGACCAAGCTCCCGTGTGAGTCCCGAGCGGTCTTCTTCTCTACAGCAAG 1260  
1261 CTACCGTGGACAGAGCAGGTGGGAGCGGTCTTCTTCTCTACAGCAAG 1320  
1261 CTACCGTGGACAGAGCAGGTGGGAGCGGTCTTCTTCTCTACAGCAAG 1320  
1321 GAGGCTCTGACCAACCACTACACGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1377  
1321 GAGGCTCTGACCAACCACTACACGAGAGCGCTCTCCCTGTCTCCGGGTAAATGA 1377

RESULT 3

US-10-860-958-1  
; Sequence 1, Application US/10860958  
; Publication No. US20040265309A1  
; GENERAL INFORMATION:  
; APPLICANT: Kandel, Jessica  
; APPLICANT: Holash, Jocelyn

APPLICANT: Yamashiro, Darrell  
APPLICANT: Huang, Jianzhong  
APPLICANT: Yancopoulos, George  
APPLICANT: Rudge, John  
TITLE OF INVENTION: Method of Tumor Regression with VEGF  
TITLE OF INVENTION: Inhibitors  
FILE REFERENCE: REG 714A  
CURRENT APPLICATION NUMBER: US/10/860,958  
PRIOR FILING DATE: 2004-06-04  
PRIOR FILING DATE: 60/476,425  
NUMBER OF SEQ ID NOS: 2  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 1377  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-860-958-1

Query Match 100.0%; Score 1377; DB 20; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGCGGCTGCTCAGCTGCTGCTTCTC 60  
Db 1 ATGCTCAGCTACTGGGACACCGGGGCTCTGCTGTGCGGCTGCTCAGCTGCTGCTTCTC 60  
Qy 61 ACAGGATCTAGTTCGGGAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCGGGAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Qy 121 CCCGAAATTAACATCATGACTGAAGAGGAGGCTCGTCTTCCCTGCGGGTTACGTCA 180  
Db 121 CCCGAAATTAACATCATGACTGAAGAGGAGGCTCGTCTTCCCTGCGGGTTACGTCA 180  
Qy 181 CCTAATCATCTGTTACTTTTAAAGGTTTCCACTGCACCTTTGATGGGAAA 240  
Db 181 CCTAATCATCTGTTACTTTTAAAGGTTTCCACTGCACCTTTGATGGGAAA 240  
Qy 241 CGCATATCTGGGACAGTGAAGGCTTCATATCATATCAATGAAGTGAAGTGAAGTGA 300  
Db 241 CGCATATCTGGGACAGTGAAGGCTTCATATCATATCAATGAAGTGAAGTGAAGTGA 300  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAACTATCTACA 360  
Db 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGACAACTATCTACA 360  
Qy 361 CATCGACAAACCAATACAATCATAGATGTGTCTGAGTCCGTCTCATGGAATTTGAAC 420  
Db 361 CATCGACAAACCAATACAATCATAGATGTGTCTGAGTCCGTCTCATGGAATTTGAAC 420  
Qy 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTTAATGTGGGAT 480  
Db 421 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTTAATGTGGGAT 480  
Qy 481 GACTTCAACTGGGAAATACCTTCTTCAAGCATCAGCATTAAGAACTTTGTAAACCGAGAC 540  
Db 481 GACTTCAACTGGGAAATACCTTCTTCAAGCATCAGCATTAAGAACTTTGTAAACCGAGAC 540  
Qy 541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTTAATATAGATGGT 600  
Db 541 CTAACAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTTAATATAGATGGT 600  
Qy 601 GTAACCCGAGTGACCAAGATTTGTACACCTGTGCGAGCATCCAGTGGGCTGATGACCAAG 660  
Db 601 GTAACCCGAGTGACCAAGATTTGTACACCTGTGCGAGCATCCAGTGGGCTGATGACCAAG 660  
Qy 661 AAGAACAGCAGATTTGTACGGGTCCATGAAAGAGCAAAACTCACACATGCCACCGTGC 720  
Db 661 AAGAACAGCAGATTTGTACGGGTCCATGAAAGAGCAAAACTCACACATGCCACCGTGC 720  
Qy 721 CCAGCACCTGAACTCTCGGGGGACCGTCAAGTCTTCTTCCCTCCCAAAACCCCAAGGAC 780  
Db 721 CCAGCACCTGAACTCTCGGGGGACCGTCAAGTCTTCTTCCCTCCCAAAACCCCAAGGAC 780









```
; CURRENT FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 10/609,775
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-880-021-9

Query Match      100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCAGCTACTGGGACACCGGGGTCCTGTCGCGCTGCTCAGCTGCTCTCTC 60
Db 1 ATGTCAGCTACTGGGACACCGGGGTCCTGTCGCGCTGCTCAGCTGCTCTCTC 60

Qy 61 ACAGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120
Db 61 ACAGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120

Qy 121 CCCGAAATTATACATGACTGAAGGAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180
Db 121 CCCGAAATTATACATGACTGAAGGAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180

Qy 181 CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGAA 240
Db 181 CCTAACATCACTGTTACTTTTAAAAAGTTTCCACTTGACACTTTTGATCCCTGATGAA 240

Qy 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATATGCAACGTACAAAGAATA 300
Db 241 CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATATGCAACGTACAAAGAATA 300

Qy 301 GGGATTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTCTCACA 360
Db 301 GGGATTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGACAAACTCTCACA 360

Qy 361 CATGACAAACCAATACAAATCATAGATGTGGTCTCTGAGTCGCTCTCATGGAAATGA 420
Db 361 CATGACAAACCAATACAAATCATAGATGTGGTCTCTGAGTCGCTCTCATGGAAATGA 420

Qy 421 TCTGTTGAGAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAATTAATGTGGGATT 480
Db 421 TCTGTTGAGAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAATTAATGTGGGATT 480

Qy 481 GACTTCAACTGGGAATACCTTCTTCCGAAGCATCAGCATAGAAACTTGTAAACCGAGAC 540
Db 481 GACTTCAACTGGGAATACCTTCTTCCGAAGCATCAGCATAGAAACTTGTAAACCGAGAC 540

Qy 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600
Db 541 CTAATAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACATATAGATGGT 600

Qy 601 GTAACCCGGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660
Db 601 GTAACCCGGAGTGACCAAGGATTTGACACCTGTGAGCATCCAGTGGGCTGATGACCAAG 660

Qy 661 AAGAACAGCATTTGTCCAGGTCATGAAAGGACAAACTCACAATGCCACCGTGC 720
Db 661 AAGAACAGCATTTGTCCAGGTCATGAAAGGACAAACTCACAATGCCACCGTGC 720

Qy 721 CCAGCACCTGAACCTCTGGGGGACCGTCACTTCTTCTTCCCGCCCAAAACCAAGGAC 780
Db 721 CCAGCACCTGAACCTCTGGGGGACCGTCACTTCTTCTTCCCGCCCAAAACCAAGGAC 780

Qy 781 ACCCTCATGATCTCCCGAACCCCTGAGGTACATGCTGCTGGTGGAGCTGAGCCAGAA 840
Db 781 ACCCTCATGATCTCCCGAACCCCTGAGGTACATGCTGCTGGTGGAGCTGAGCCAGAA 840

Qy 841 GACCTGAGGTCAAGTTTCACTGGTACGTGGACGCGTGGAGGTGCATTAATGCCAAGACA 900
Db 121 GACCTGAGGTCAAGTTTCACTGGTACGTGGACGCGTGGAGGTGCATTAATGCCAAGACA 180
```

```
Db 841 GACCTGAGGTCAAGTTTCACTGGTACGTGGACGCGTGGAGGTGCATTAATGCCAAGACA 900
Qy 901 AAGCCCGGGAGGAGCAGTACAACAGCAGTACCGTGTGTGTGTCAGCGTCTCTACCGTCTG 960
Db 901 AAGCCCGGGAGGAGCAGTACAACAGCAGCAGTACCGTGTGTGTGTCAGCGTCTCTACCGTCTG 960
Qy 961 CACCAGGACTGGCTGTAATGCAAGGAGTACAAGTGAAGGTCTTCCAAAGAGCCCTCCCA 1020
Db 961 CACCAGGACTGGCTGTAATGCAAGGAGTACAAGTGAAGGTCTTCCAAAGAGCCCTCCCA 1020
Qy 1021 GCCCCCATCGAGAAACCATCTTCCAAAGCCAAAGGGCAGCCCCGAGAACACACAGTGTAC 1080
Db 1021 GCCCCCATCGAGAAACCATCTTCCAAAGCCAAAGGGCAGCCCCGAGAACACACAGTGTAC 1080
Qy 1081 ACCCTGCCCCATCCCGGATGAGTGAACAAAGAACAGGTGACCTGACCTGCTGGTC 1140
Db 1081 ACCCTGCCCCATCCCGGATGAGTGAACAAAGAACAGGTGACCTGACCTGCTGGTC 1140
Qy 1141 AAAGGCTTCTATCCACGGACATCGCGTGGAGTGGGAGAGCAATGGCGAGCCGGAAC 1200
Db 1141 AAAGGCTTCTATCCACGGACATCGCGTGGAGTGGGAGAGCAATGGCGAGCCGGAAC 1200
Qy 1201 AACTACAAGACCAAGCTCCGCTGCTGACTCCGACGGCTCTTCTTCTCTACAGCAAG 1260
Db 1201 AACTACAAGACCAAGCTCCGCTGCTGACTCCGACGGCTCTTCTTCTCTACAGCAAG 1260
Qy 1261 CTCACTGTGACAAAGAGCAGTGGCAGCAGGGGAACTCTTCTCATGCTCCGTGATGCAT 1320
Db 1261 CTCACTGTGACAAAGAGCAGTGGCAGCAGGGGAACTCTTCTCATGCTCCGTGATGCAT 1320
Qy 1321 GAGGCTCTGCACACCACTACACGACAGAGCTCTCCCTGTCTCCGGGTAAATGA 1377
Db 1321 GAGGCTCTGCACACCACTACACGACAGAGCTCTCCCTGTCTCCGGGTAAATGA 1377
```

## RESULT 7

```
US-10-909-011-3
; Sequence 3, Application US/10909011
; Publication No. US2005012061A1
; GENERAL INFORMATION:
; APPLICANT: Jocelyn Holash
; APPLICANT: George Yancopoulos
; APPLICANT: Phyllis R. Wachberger
; APPLICANT: Adam P. Dickler
; APPLICANT: Randy Burd
; TITLE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy
; FILE REFERENCE: REG 716A
; CURRENT APPLICATION NUMBER: US/10/909,011
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: 60/492,864
; PRIOR FILING DATE: 2003-08-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1377
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-909-011-3
```

```
Query Match      100.0%; Score 1377; DB 21; Length 1377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCAGCTACTGGGACACCGGGGTCCTGTCGCGCTGCTCAGCTGCTCTCTC 60
Db 1 ATGTCAGCTACTGGGACACCGGGGTCCTGTCGCGCTGCTCAGCTGCTCTCTC 60

Qy 61 ACAGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120
Db 61 ACAGATCTAGTTCGGGAGTGTACCGGTAGACCTTTCGTAGAGATGACAGTGAATC 120

Qy 121 CCCCCAAATTATACATGACTGAAGGAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180
Db 121 CCCCCAAATTATACATGACTGAAGGAGGAGCTCGTCATTCCCTGCGGGTTACGTCA 180
```

Db 121 CCAGAAATTTATACATGACTGAAGGAGGGAGCTCGTCATTCCCTCGCGGGTTACGTCA 180  
Qy 181 CTTAAACATCAGCTGTTACTTTAAAGAGTTTCCACTTGCACACTTTGATCCCTGATGAAAA 240  
Db 181 CTTAAACATCAGCTGTTACTTTAAAGAGTTTCCACTTGCACACTTTGATCCCTGATGAAAA 240  
Qy 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 300  
Db 241 CGCATAATCTGGGACAGTAGAAGGGCTTCATCATATCAAAATGCAACGTACAAAGAAATA 300  
Qy 301 GGGCTTCTGACCTGTGAAGCAACGTCAATGGGCAATTTGTATAGCAAACTATCTCACA 360  
Db 301 GGGCTTCTGACCTGTGAAGCAACGTCAATGGGCAATTTGTATAGCAAACTATCTCACA 360  
Qy 361 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATGAACATA 420  
Db 361 CATCGACAAACCAATACAAATCATAGATGTGGTTCTGAGTCCGTCTCATGGAATGAACATA 420  
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480  
Db 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480  
Qy 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAACTTTGTAACCGGAC 540  
Db 481 GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAACTTTGTAACCGGAC 540  
Qy 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGT 600  
Db 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACATATAGATGGT 600  
Qy 601 GTAAACCGGAGTGACCAAGGATTTGACCTGTGACGATCCAGTGGGCTGATGACCAAG 660  
Db 601 GTAAACCGGAGTGACCAAGGATTTGACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Qy 661 AAGACAGACATTTGTGAGGTTCATGAAAGGACAAACTCAACATGCCACCGTGC 720  
Db 661 AAGACAGACATTTGTGAGGTTCATGAAAGGACAAACTCAACATGCCACCGTGC 720  
Qy 721 CCAGCACCTGAACTCTCGGGGGACCGTCAGTCTTCTTCCCCCAAAACCCAAAGGAC 780  
Db 721 CCAGCACCTGAACTCTCGGGGGACCGTCAGTCTTCTTCCCCCAAAACCCAAAGGAC 780  
Qy 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAA 840  
Db 781 ACCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGAGCGTGAGCCACGAA 840  
Qy 841 GACCTGAGGTCAAGTTCACTGCTGACGTGACGCGGTGGAGGTGCATAATGCCAAGACA 900  
Db 841 GACCTGAGGTCAAGTTCACTGCTGACGTGACGCGGTGGAGGTGCATAATGCCAAGACA 900  
Qy 901 AAGCCGCGGAGGAGCAGTACAAACGACGCTACCGTGTGGTCCGCTCTCACCGTCTGT 960  
Db 901 AAGCCGCGGAGGAGCAGTACAAACGACGCTACCGTGTGGTCCGCTCTCACCGTCTGT 960  
Qy 961 CAACAGGACTGGCTGAAATGGCAAGGAGTACAAGTGCAGAGTCTCCACAAAGCCCTCCA 1020  
Db 961 CAACAGGACTGGCTGAAATGGCAAGGAGTACAAGTGCAGAGTCTCCACAAAGCCCTCCA 1020  
Qy 1021 GCCTCCATCGAGAAACCATCTCCAAAGCCAAAGGGGAGCCCGGAGAACCAAGGTGTAC 1080  
Db 1021 GCCTCCATCGAGAAACCATCTCCAAAGCCAAAGGGGAGCCCGGAGAACCAAGGTGTAC 1080  
Qy 1081 ACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTGTACCTGACCTGCTGTGTC 1140  
Db 1081 ACCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAAGGTGTACCTGACCTGCTGTGTC 1140  
Qy 1141 AAAGGCTTTCTATCCAGAGCATCGCGTGGAGTGGGAGAGCAATGGGACGCCGAGAAC 1200  
Db 1141 AAAGGCTTTCTATCCAGAGCATCGCGTGGAGTGGGAGAGCAATGGGACGCCGAGAAC 1200  
Qy 1201 AACTACAAAGACAGCGCTCCGCTGTGATGATCCGACGGCTCTTCTTCTCTACAGCAAG 1260  
Db 1201 AACTACAAAGACAGCGCTCCGCTGTGATGATCCGACGGCTCTTCTTCTCTACAGCAAG 1260

RESULT 8

US-10-988-243-15  
; Sequence 15, Application US/10988243  
; Publication No. US20050175610A1  
; GENERAL INFORMATION:  
; APPLICANT: Wiegand, Stanley  
; APPLICANT: Papadopoulos, Nicholas J.  
; APPLICANT: Yancopoulos, George  
; TITLE OF INVENTION: Modified Chimeric Polypeptides with Improved Pharmacokinetic Properties  
; TITLE OF INVENTION: and Methods of Making and Using Thereof  
; FILE REFERENCE: REG 710F  
; CURRENT APPLICATION NUMBER: US/10/988,243  
; CURRENT FILING DATE: 2004-11-12  
; PRIOR APPLICATION NUMBER: 10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15  
; LENGTH: 1377  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-988-243-15

Query Match 100.0%; Score 1377; DB 22; Length 1377;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTCGCGGCTGCTCAGCTGCTCTCTCTC 60  
Db 1 ATGTCAGCTACTGGGACACCGGGTCTCTGTCGCGGCTGCTCAGCTGCTCTCTCTC 60  
Qy 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Db 61 ACAGGATCTAGTTCCGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC 120  
Qy 121 CCGGAAATTTATACATGACTGAAGGAAGGAGCTCGTCATTCCCTCGCGGGTTACGTCA 180  
Db 121 CCGGAAATTTATACATGACTGAAGGAAGGAGCTCGTCATTCCCTCGCGGGTTACGTCA 180  
Qy 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGAAAA 240  
Db 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGAAAA 240  
Qy 241 CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAACGTACAAAGAAATA 300  
Db 241 CGCATATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAACGTACAAAGAAATA 300  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGCAAACTATCTCACA 360  
Db 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAGCAAACTATCTCACA 360  
Qy 361 CATCGACAAACCAATACAAATCATAGATGTGGTCTGAGTCCGTCTCATGGAATGAACATA 420  
Db 361 CATCGACAAACCAATACAAATCATAGATGTGGTCTGAGTCCGTCTCATGGAATGAACATA 420  
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480  
Db 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACCTAAATGTGGGATT 480









US-10-880-021-7  
; Sequence 7, Application US/10880021  
; Publication No. US20050043236A1  
; GENERAL INFORMATION:  
; APPLICANT: Daly, Thomas J.  
; APPLICANT: Fandi, James P.  
; APPLICANT: Papadopoulos, Nicholas J.  
; FILE OF INVENTION: VEGF Traps and Therapeutic Uses Thereof  
; CURRENT APPLICATION NUMBER: US/10/880,021  
; FILE REFERENCE: RGE 710D2  
; CURRENT FILING DATE: 2004-06-29  
; PRIOR APPLICATION NUMBER: 10/609,775  
; PRIOR FILING DATE: 2003-06-30  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 7  
; LENGTH: 1453  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-880-021-7

Query Match 96.5%; Score 1328.4; DB 21; Length 1453;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;

QY 1 ATGTCAGCTACTGGGACACCGGGTCTCTGCTGCGCGCTGCTCAGCTGTCTGCTTCTC 60  
DB |||||  
69 ATGTCAGCTACTGGGACACCGGGTCTCTGCTGCGCGCTGCTCAGCTGTCTGCTTCTC 128  
QY 61 ACAGGATCTAGTTCGGAGTATACCGGTAGACCTTTGCTAGAGATGTACAGTGAATC 120  
DB |||||  
129 ACAGGATCTAGTTCGGAGTATACCGGTAGACCTTTGCTAGAGATGTACAGTGAATC 179  
QY 121 CCAGAAATATACATGACTGAAGGAGGAGCTCGTCAATTCCTCGCGGGTACGTCA 180  
DB |||||  
180 CCAGAAATATACATGACTGAAGGAGGAGCTCGTCAATTCCTCGCGGGTACGTCA 239  
QY 181 CTAACATCACTGTACTTTAAAAAGTTTCCACTTTGACACATTTGATCCCTGATGAAAA 240  
DB |||||  
240 CTAACATCACTGTACTTTAAAAAGTTTCCACTTTGACACATTTGATCCCTGATGAAAA 299  
QY 241 CGATAATCTGGACATGAGAAAGGCTTCATCATATCAATATGCAACGTACAAAGAAAT 300  
DB |||||  
300 CGATAATCTGGACATGAGAAAGGCTTCATCATATCAATATGCAACGTACAAAGAAAT 359  
QY 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTACA 360  
DB |||||  
360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTACA 419  
QY 361 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGCTCATGGAATTGAACATA 420  
DB |||||  
420 CATCGACAAACCAATACATATAGATGTGTTCTGAGTCCGCTCATGGAATTGAACATA 479  
QY 421 TCTGTTGGAGAAAGCTTCTTAAATTTGTAAGCAAGAACTGAACTAAATGTGGGAT 480  
DB |||||  
480 TCTGTTGGAGAAAGCTTCTTAAATTTGTAAGCAAGAACTGAACTAAATGTGGGAT 539  
QY 481 GACTTCACTGGGAATACCTTCTCGAGCATCAGCATAGAACTTTGTAACCGAGAC 540  
DB |||||  
540 GACTTCACTGGGAATACCTTCTCGAGCATCAGCATAGAACTTTGTAACCGAGAC 599  
QY 541 CTAACAAACCCAGTCTGGGAGTGAAGAAATTTTGGACACCTTAACATATAGATG 600  
DB |||||  
600 CTAACAAACCCAGTCTGGGAGTGAAGAAATTTTGGACACCTTAACATATAGATG 659  
QY 601 GTAACCCGAGTGAACAGGATTTACCTGTGAGCATCAGTGGGCTGATGACCAAG 660  
DB |||||  
660 GTAACCCGAGTGAACAGGATTTACCTGTGAGCATCAGTGGGCTGATGACCAAG 719  
QY 661 AAGACACGACATTTGTGAGGTCATGAAAG-----GACAAACTCACACATGC 711  
DB |||||  
720 AAGACACGACATTTGTGAGGTCATGAAAGGGCCCGGGCGACAAAACTCACACATGC 779

QY 712 CCACCGTCCCAGCAGCACTGAACTCTCTGGGGGACCGTCACTTCTCTTCCCTCCCAAAA 771  
DB |||||  
780 CCACCGTCCCAGCAGCACTGAACTCTCTGGGGGACCGTCACTTCTCTTCCCTCCCAAAA 839  
QY 772 CCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTG 831  
DB |||||  
840 CCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTG 899  
QY 832 AGCCACGAAGACCCCTGAGGTCAAGTTCACTGGTGAAGCGGCGTGGAGGTGATAT 891  
DB |||||  
900 AGCCACGAAGACCCCTGAGGTCAAGTTCACTGGTGAAGCGGCGTGGAGGTGATAT 959  
QY 892 GCCAAGACAAAGCCCGGAGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCGTCTC 951  
DB |||||  
960 GCCAAGACAAAGCCCGGAGAGCAGTACAAACAGCAGTACCGTGTGGTCAAGCGTCTC 1019  
QY 952 ACCGTCCTGCAACGAGGACTGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAACA 1011  
DB |||||  
1020 ACCGTCCTGCAACGAGGACTGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAACA 1079  
QY 1012 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1071  
DB |||||  
1080 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAAGCCAAAGGCGAGCCCGGAGAACCA 1139  
QY 1072 CAGGTGTACACCCCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTCAAGCCTGACC 1131  
DB |||||  
1140 CAGGTGTACACCCCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTCAAGCCTGACC 1199  
QY 1132 TGCTGTGTAAGGGTTCTATCCAGCGACATTCGCCGTGGAGTGGGAGAGCAATGGGAG 1191  
DB |||||  
1200 TGCTGTGTAAGGGTTCTATCCAGCGACATTCGCCGTGGAGTGGGAGAGCAATGGGAG 1259  
QY 1192 CCGGAGAACAACTACAAGCACCGCTCCCGTGTGGAATCCGAGCGGTCTCTTCTTCTC 1251  
DB |||||  
1260 CCGGAGAACAACTACAAGCACCGCTCCCGTGTGGAATCCGAGCGGTCTCTTCTTCTC 1319  
QY 1252 TACAGCAGCTCACCGTGGACAAAGCAGAGTGGCAGCAGGGGAAAGCTTCTCATGCTCC 1311  
DB |||||  
1320 TATAGCAGCTCACCGTGGACAAAGCAGAGTGGCAGCAGGGGAAAGCTTCTCATGCTCC 1379  
QY 1312 GTGATGATAGGCTCTGCAACCACTACAGCGAGAAAGAGCCTTCCCTGTCTCCGGGT 1371  
DB |||||  
1380 GTGATGATAGGCTCTGCAACCACTACAGCGAGAAAGAGCCTTCCCTGTCTCCGGGT 1439  
QY 1372 AAATGA 1377  
DB |||||  
1440 AAATGA 1445

RESULT 13  
US-10-909-011-1  
; Sequence 1, Application US/10909011  
; Publication No. US20050112061A1  
; GENERAL INFORMATION:  
; APPLICANT: Jocelyn Holash  
; APPLICANT: George Yancopoulos  
; APPLICANT: Phyllis R. Wacheberger  
; APPLICANT: Adam P. Dicker  
; APPLICANT: Randy Burd  
; FILE OF INVENTION: Use of a VEGF Antagonist in Combination with Radiation Therapy  
; FILE REFERENCE: REG 716A  
; CURRENT APPLICATION NUMBER: US/10/909,011  
; CURRENT FILING DATE: 2004-07-30  
; PRIOR APPLICATION NUMBER: 60/492,864  
; PRIOR FILING DATE: 2003-08-06  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1453  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-909-011-1



Query Match		96.5%;	Score 1328.4;	DB 21;	Length 1453;
Best Local Similarity		98.6%;	Pred. No. 0;		
Matches 1367;		Conservative	0;	Mismatches	1; Indels 18; Gaps 2;
Qy	1	ATGCTCAGCTACTGGGACACCGGGGTCTGTGTGCGGCTGCTCAGCTGTCTGCTTCTC	60		
Db	69	ATGCTCAGCTACTGGGACACCGGGGTCTGTGTGCGGCTGCTCAGCTGTCTGCTTCTC	128		
Qy	61	ACAGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTCGTAGAGATGTACAGTGAATC	120		
Db	129	ACAGATCTAGTTCGGGA-----GGTAGACCTTTTCGTAGAGATGTACAGTGAATC	179		
Qy	121	CCCGAAATTATACACATCACTGAAAGGAGGAGCTGCTCATTTCCCTGCGGGTTACGTCA	180		
Db	180	CCCGAAATTATACATCACTGAAAGGAGGAGCTGCTCATTTCCCTGCGGGTTACGTCA	239		
Qy	181	CCTAACATCACTGTTTACTTTAAAAAGTTTCCACTTGGACACTTTTGATCCCTGATGGAAA	240		
Db	240	CCTAACATCACTGTTTACTTTAAAAAGTTTCCACTTGGACACTTTTGATCCCTGATGGAAA	299		
Qy	241	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAAAGAATA	300		
Db	300	CGCATATCTGGGACAGTAGAAGGGCTTCATCATATCAATGCAACGTACAAAGAATA	359		
Qy	301	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTGTATAGACAAACTATCTCACA	360		
Db	360	GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTGTATAGACAAACTATCTCACA	419		
Qy	361	CATGACAAACCAATACATATAGATGTGGTCTTGAGTCCGTCTCATGGAATTTGAACCTA	420		
Db	420	CATGACAAACCAATACATATAGATGTGGTCTTGAGTCCGTCTCATGGAATTTGAACCTA	479		
Qy	421	TCTGTGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGATT	480		
Db	480	TCTGTGAGAAAAGCTTGTCTTAAATTGTACAGCAAGAACTGAACTAAATGTGGGATT	539		
Qy	481	GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAACTTGTAAACCGGAGAC	540		
Db	540	GACTTCAACTGGGAATACCTTCTTCGAAGCATCAGCATAGAACTTGTAAACCGGAGAC	599		
Qy	541	CTAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGGT	600		
Db	600	CTAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGTAGCACCTTAACTATAGATGGT	659		
Qy	601	GTAACCCGGAGTACCAGGATTTGACACCTGTGCGAGCATCCAGTGGCTGATACCAAG	660		
Db	660	GTAACCCGGAGTACCAGGATTTGACACCTGTGCGAGCATCCAGTGGGCTGATGACCAAG	719		
Qy	661	AAGAACAGACATTTGTCAAGGTCCATGAAAAG-----GACAAACTCACACATGC	711		
Db	720	AAGAACAGACATTTGTCAAGGTCCATGAAAAGGGCCCGGGCGACAAACTCACACATGC	779		
Qy	712	CCACCGTCCGACGACCTTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCCCAAAA	771		
Db	780	CCACCGTCCGACGACCTTGAATCTCTGGGGGACCGTCAAGTCTTCTCTTCCCGCCCAAAA	839		
Qy	772	CCCAAGGACACCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGGTGGAGCGTG	831		
Db	840	CCCAAGGACACCCCTCATGATCTCCCGGACCCCTGAGGTCAATGCTGGTGGTGGAGCGTG	899		
Qy	832	AGCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGCTGGAGGTGCATAAT	891		
Db	900	AGCACGAAGACCCCTGAGGTCAAGTTCAACTGGTACGTGGACGCGCTGGAGGTGCATAAT	959		
Qy	892	GCCAAGACAAAGCCCGGGAGGACAGTACAACAGCACGTACCGTGTGGTCAAGCTCTC	951		
Db	960	GCCAAGACAAAGCCCGGGAGGACAGTACAACAGCACGTACCGTGTGGTCAAGCTCTC	1019		
Qy	952	ACCGTCTCTGACAGGACTGCTGAAATGGCAAGGATCAAGTCCAGGCTCTCAACAA	1011		
Db	1020	ACCGTCTCTGACAGGACTGCTGAAATGGCAAGGATCAAGTCCAGGCTCTCAACAA	1079		
Qy	1012	GCCCTCCAGGCCCCCATCGAGAAAACCATCTCCAAAGCAAAGGCGACCCCGGAGAACCA	1071		

Db	1080																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												</
----	------	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	----

Db 240 CCTAACATCATCTGTTACTTTAAAAAGTTTCCACTTGCACACTTTTGATCCCTGATGAAAA 299  
Qy 241 CGATAAATCTGGGACAGTAGAAGGCTTTCATCATATCAAAATGCAACCTGACAAAGAAATA 300  
Db 300 CGCATTAATCTGGACAGTAGAAGGCTTTCATCATATCAAAATGCAACCTGACAAAGAAATA 359  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGCTCAATGGGCAATTTGTATAAGCAAAACTATCTCACA 360  
Db 360 GGGCTTCTGACCTGTGAAGCAACAGCTCAATGGGCAATTTGTATAAGCAAAACTATCTCACA 419  
Qy 361 CATCGACAAACCAATACATATCATAGATGTTCTGAGTCCGTCTCATGGAATGAACTA 420  
Db 420 CATCGACAAACCAATACATATCATAGATGTTCTGAGTCCGTCTCATGGAATGAACTA 479  
Qy 421 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAAGTAAATGTTGGGAT 480  
Db 480 TCTGTTGAGAAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAAGTAAATGTTGGGAT 539  
Qy 481 GACTTCAACTGGGAATACCCCTTCTTGAAGCATACAGCATAGAAACTTTGTAAACCGAGAC 540  
Db 540 GACTTCAACTGGGAATACCCCTTCTTGAAGCATACAGCATAGAAACTTTGTAAACCGAGAC 599  
Qy 541 CTNAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTCAGCACCTTAACCTATAGATGGT 600  
Db 600 CTNAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTTCAGCACCTTAACCTATAGATGGT 659  
Qy 601 GTAAACCCGAGTGACCAAGGATTTGACACCTGTGACGATCCAGTGGGCTCATGACCAAG 660  
Db 660 GTAAACCCGAGTGACCAAGGATTTGACACCTGTGACGATCCAGTGGGCTCATGACCAAG 719  
Qy 661 AAGAACAGCACATTTGTGAGGTCATGAAAG-----GACAAAACTCACACATGC 711  
Db 720 AAGAACAGCACATTTGTGAGGTCATGAAAGGGCCCGGGCGACAAAACTCACACATGC 779  
Qy 712 CCACGCTGCCAGACACTGAACCTCTCGGGGAGCGCTCAGTCTTCTTCCCGCCAAA 771  
Db 780 CCACGCTGCCAGACACTGAACCTCTCGGGGAGCGCTCAGTCTTCTTCCCGCCAAA 839  
Qy 772 CCCAAGGACACCTCTATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTG 831  
Db 840 CCCAAGGACACCTCTATGATCTCCCGGACCCCTGAGGTACATGCGTGGTGGAGCTG 899  
Qy 832 AGdCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGCGGCGGTGGAGGTGCATAAT 891  
Db 900 AGdCACGAAGACCTTGAGGTCAAGTTCAACTGGTACGCGGCGGTGGAGGTGCATAAT 959  
Qy 892 GdCAAGACAAAGCCCGGGAGAGCAGTACAAACAGCAGTACCGTGGTGGTCCCTC 951  
Db 960 GdCAAGACAAAGCCCGGGAGAGCAGTACAAACAGCAGTACCGTGGTGGTCCCTC 1019  
Qy 952 ACCGTCTCTGACACGAGTCTGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAACAA 1011  
Db 1020 ACCGTCTCTGACACGAGTCTGCTGAATGGCAAGGAGTACAAAGTCAAGGTCTCCAAACAA 1079  
Qy 1012 GdCTTCCAGCCCGCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACCA 1071  
Db 1080 GdCTTCCAGCCCGCCATCGAGAAAACCATCTCCAAAGCCAAAGGCGACGCCCGGAGAACCA 1139  
Qy 1072 CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCTGACC 1131  
Db 1140 CAGGTGTACACCTGCCCCCATCCCGGATGAGCTGACCAAGAACAGGTGAGCTGACC 1199  
Qy 1132 TGCTTGGTCAAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGAG 1191  
Db 1200 TGCTTGGTCAAAAGGCTTCTATCCAGCGACATCCCGTGGAGTGGAGAGCAATGGGCGAG 1259  
Qy 1192 CCGGAGAAACAACTACAAGACCAAGCTCCCGTGGTGGACTCCGACGGCTCTTCTTCTC 1251  
Db 1260 CCGGAGAAACAACTACAAGACCAAGCTCCCGTGGTGGACTCCGACGGCTCTTCTTCTC 1319  
Qy 1252 TACAGCAAGCTCAACGTTGGACAAGAGCAGGTGGGACAGGGGAAACGCTTCTCATGCTCC 1311  
Db 1320 TATAGCAAGCTCACCGTTGGACAAGAGCAGGTGGGACAGGGGAAACGCTTCTCATGCTCC 1379

Qy 1312 GTGATGATGAGGCTCTGCACCAACACTACACGAGAGAGCCCTCTCCCTGCTCCGGGT 1371  
Db 1380 GTGATGATGAGGCTCTGCACCAACACTACACGAGAGAGCCCTCTCCCTGCTCCGGGT 1439  
Qy 1372 AAATGA 1377  
Db 1440 AAATGA 1445  
RESULT 15  
US-11-016-097-11  
; Sequence 11, Application US/11016097  
; Publication No. US20050163798A1  
; GENERAL INFORMATION:  
; APPLICANT: Nicholas J. Papadopoulos et al.  
; TITLE OF INVENTION: MODIFIED CHIMERIC POLYPEPTIDES WITH IMPROVED  
; TITLE OF INVENTION: PHARMACOKINETIC PROPERTIES AND METHODS OF MAKING  
; TITLE OF INVENTION: AND USING THEREOF  
; FILE REFERENCE: REG 710-A-US  
; CURRENT APPLICATION NUMBER: US/11/016,097  
; CURRENT FILING DATE: 2004-12-17  
; PRIOR APPLICATION NUMBER: US/10/009,852  
; PRIOR FILING DATE: 2001-12-06  
; PRIOR APPLICATION NUMBER: PCT/US00/14142  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/138,133  
; PRIOR FILING DATE: 1999-06-08  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 1453  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (69)...(1442)  
US-11-016-097-11

Query Match 96.5%; Score 1328.4; DB 24; Length 1453;  
Best Local Similarity 98.6%; Pred. No. 0;  
Matches 1367; Conservative 0; Mismatches 1; Indels 18; Gaps 2;  
Qy 1 ATGCTCAGCTACTGGGACACCGGGTCTCTGCTGCGCGCTGCTCAGCTGCTGCTCTC 60  
Db 69 ATGCTCAGCTACTGGGACACCGGGTCTCTGCTGCGCGCTGCTCAGCTGCTGCTCTC 128  
Qy 61 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGACCTTTTCGTAGAGATGTACAGTGAATC 120  
Db 129 ACAGGATCTAGTTCGGGAAGTGATACCGGTAGAGATGTACAGTGAATC 179  
Qy 121 CCGGAAATTTATACATGATCTGAAGGAGGAGTCTGCTCCTCCCGGGTTACGTCA 180  
Db 180 CCGGAAATTTATACATGATCTGAAGGAGGAGTCTGCTCCTCCCGGGTTACGTCA 239  
Qy 181 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 240  
Db 240 CCTAACATCACTGTTACTTTAAAAAGTTTCCACTTGACACTTTGATCCCTGATGGAATA 299  
Qy 241 CGCATAAATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAACGTACAAAGAAATA 300  
Db 300 CGCATAAATCTGGGACAGTAGAAGGGTTCATCATATCAAAATGCAACGTACAAAGAAATA 359  
Qy 301 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCACA 360  
Db 360 GGGCTTCTGACCTGTGAAGCAACAGTCAATGGGCAATTTGTATAAGCAAACTATCTCACA 419  
Qy 361 CATCGACAAACCAATACAATCATAGATGTTCTGAGTCCGTCTCATGGAATGAACTA 420  
Db 420 CATCGACAAACCAATACAATCATAGATGTTCTGAGTCCGTCTCATGGAATGAACTA 479  
Qy 421 TCTGTTGGAGAAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAAGTAAATGTTGGGAT 480

Db 480 TCTGTTGGAGAAAGCTTGTCTTAAATTTGTACAGCAAGAACTGAACATAAATGTGGGATT 539  
QY 481 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 540  
Db 540 GACTTCAACTGGGAATACCTTCTTGAAGCATCAGCATAGAAACTTTGTAAACCGAGAC 599  
QY 541 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACCTATAGATGGT 600  
Db 600 CTAAAAACCCAGTCTGGGAGTGAGATGAAGAAATTTTGGACACCTTAACCTATAGATGGT 659  
QY 601 GTAAACCCGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 660  
Db 660 GTAAACCCGAGTGACCAAGGATTGTACACCTGTGCAGCATCCAGTGGGCTGATGACCAAG 719  
QY 661 AAGAACAGACATTTGTGAGGGTCCATGAAAG-----GACAAAACTCACACATGC 711  
Db 720 AAGAACAGACATTTGTGAGGGTCCATGAAAGGGCCCGGGCGACAAAACTCACACATGC 779  
QY 712 CCACCGTGCCAGACACCTGAACTCCTGGGGGAGCCGTGAGTCTTCTCTTCCCCCAAAA 771  
Db 780 CCACCGTGCCAGACACCTGAACTCCTGGGGGAGCCGTGAGTCTTCTCTTCCCCCAAAA 839  
QY 772 CCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTG 831  
Db 840 CCCAAGGACACCCCTCATGATCTCCGGACCCCTGAGGTCAATGCGTGGTGGTGGACGTG 899  
QY 832 AGCCACGAAGACCTGAGGTCAAGTTCAACTGTTACGTGGAAGGCGGTGGAGGTGCATAT 891  
Db 900 AGCCACGAAGACCTGAGGTCAAGTTCAACTGTTACGTGGAAGGCGGTGGAGGTGCATAT 959  
QY 892 GCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGTCAGGTCCTC 951  
Db 960 GCCAAGACAAAGCCGCGGAGGAGCAGTACAACAGCAGTACCGTGTGTCAGGTCCTC 1019  
QY 952 ACCGTCTGTCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAA 1011  
Db 1020 ACCGTCTGTCACAGGACTGGCTGAATGGCAAGGAGTACAAGTCAAGGTCTCCAACAAA 1079  
QY 1012 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCCAAAGGCGAGCCCCGAGAACCA 1071  
Db 1080 GCCCTCCAGCCCCCATCGAGAAACCATCTCCAAGCCAAAGGCGAGCCCCGAGAACCA 1139  
QY 1072 CAGGTGTACACCTGCCGCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACC 1131  
Db 1140 CAGGTGTACACCTGCCGCCCATCCCGGATGAGCTGACCAAGAACCCAGGTCAAGCTGACC 1199  
QY 1132 TGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAG 1191  
Db 1200 TGCCTGGTCAAAGGCTTCTATCCAGCGACATCGCGTGGAGTGGGAGAGCAATGGGCGAG 1259  
QY 1192 CCGGAGAACAACTACAAGACCAAGCCTCCCGTGGTGGACTCGGAGGGCTCCTTCTTCTC 1251  
Db 1260 CCGGAGAACAACTACAAGACCAAGCCTCCCGTGGTGGACTCGGAGGGCTCCTTCTTCTC 1319  
QY 1252 TACAGCAAGCTCACCGTGACAGAGAGTGGCAGAGGGGAAAGCTCTTCTCATGTCTCC 1311  
Db 1320 TATAGCAAGCTCACCGTGACAGAGAGTGGCAGAGGGGAAAGCTCTTCTCATGTCTCC 1379  
QY 1312 GTGATGCATGAGGCTCTGCACAAACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGT 1371  
Db 1380 GTGATGCATGAGGCTCTGCACAAACCACTACACGCAAGAGAGCCTCTCCCTGTCTCCGGGT 1439  
QY 1372 AAATGA 1377  
Db 1440 AAATGA 1445